

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 11:57:54 ; Search time 5416 Seconds
(without alignments)
10453.486 Million cell updates/sec

Title: US-10-723-947-75

Perfect score: 996

Sequence: 1 taactgcctctctcttctcc.....tagctacttgatgtgtaat 996

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5893141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_in.*

3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pt.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vl.*

14: gb_btg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	848.4	85.2	850	15	AY485965	AY485965 Triticum
2	848.4	85.2	850	15	AY485966	AY485966 Triticum
3	848.4	85.0	850	15	AY485968	AY485968 Triticum
4	846.8	85.0	850	15	AY485967	AY485967 Triticum
5	830.8	83.4	847	15	AY485964	AY485964 Triticum
6	830.8	83.4	850	15	AY485963	AY485963 Triticum
7	776	77.9	792	15	AY485969	AY485969 Triticum
8	561	56.3	110000	15	AY485644_3	Continuation (4 of AY485644_3)
9	464.4	46.6	712	15	AY485975	AY485975 Triticum
10	464.4	46.6	712	15	AY485976	AY485976 Triticum
11	420	42.2	2078	15	AY485979	AY485979 Triticum
12	320.8	32.2	110000	15	AY485644_2	Continuation (3 of AY485644_2)
13	267.2	26.8	1790	15	AY485980	AY485980 Triticum
14	251.4	25.2	2064	15	AY485978	AY485978 Hordeum v
15	247.6	24.9	1985	15	AY485977	AY485977 Hordeum v
16	206.4	20.7	264	15	AY687931	AY687931 Hordeum v
17	157	15.8	687	15	AY485970	AY485970 Triticum
18	157	15.8	687	15	AY485971	AY485971 Triticum

19	152.2	15.3	688	15	AY485972	AY485972 Triticum
20	137.6	13.8	834	15	AY485973	AY485973 Triticum
C 21	93	9.3	110000	15	AP008213	Continuation (92 of AP008213)
C 22	93	9.3	150554	15	AP005307	AP005307 Oryza sat
23	88.2	8.9	944	15	AY082965	AY082965 Hordeum v
24	86	8.6	1258	15	AK109732	AK109732 Oryza sat
C 25	86	8.6	110000	15	AP008216	Continuation (216 of AP008216)
26	86	8.6	144191	15	AC079874	AC079874 Oryza sat
C 27	86	8.6	300029	15	AE017119	AE017119 Oryza sat
28	79	7.9	1534	15	AY485974	AY485974 Triticum
29	76.6	7.7	885	6	AX050570	AX050570 Sequence
30	76.6	7.7	990	15	BT002107	BT002107 Arabidops
31	76.6	7.7	1103	15	AY140103	AY140103 Arabidops
32	76.6	7.7	1124	15	AY085729	AY085729 Arabidops
33	76.6	7.7	1127	15	AY058130	AY058130 Arabidops
34	76.6	7.7	6237	15	AC007266	AC007266 Arabidops
C 35	76.6	7.7	103495	15	AC006585	AC006585 Arabidops
36	75.6	7.6	1163	15	AY082960	AY082960 Hordeum v
37	75.6	7.6	1324	15	AY082962	AY082962 Hordeum v
38	75.6	7.6	1455	15	AY082961	AY082961 Hordeum v
C 39	75.4	7.6	110000	15	AP008212	Continuation (265 of AP008212)
C 40	75.4	7.6	170964	15	AP003579	AP003579 Oryza sat
41	74.8	7.5	1396	15	AK121024	AK121024 Oryza sat
42	74.8	7.5	110000	15	AP008210	Continuation (249 of AP008210)
43	74.8	7.5	170765	15	OSJN00052	AL606627 Oryza sat
44	74.6	7.5	1386	15	AK100097	AK100097 Oryza sat
45	74.6	7.5	1388	15	AK058536	AK058536 Oryza sat

ALIGNMENTS

RESULT 1	AY485965	AY485965	850 bp	mrna	linear	PUN 17-MAR-2004
LOCUS	AY485965	Triticum monococcum cultivar PI272561	ZCCT1 (VRN2)	mrna	complete	
DEFINITION	AY485965	Triticum monococcum cultivar PI272561	ZCCT1 (VRN2)	mrna	complete	
ACCESSION	AY485965	AY485965.1	GI:45390685			
VERSION	AY485965	AY485965.1	GI:45390685			
KEYWORDS	AY485965	Triticum monococcum				
SOURCE	AY485965	Triticum monococcum				
ORGANISM	AY485965	Triticum monococcum				
REFERENCE	AY485965	Triticum monococcum				
AUTHORS	AY485965	Triticum monococcum				
TITLE	AY485965	Triticum monococcum				
JOURNAL	AY485965	Triticum monococcum				
PUBMED	AY485965	Triticum monococcum				
REFERENCE	AY485965	Triticum monococcum				
AUTHORS	AY485965	Triticum monococcum				
TITLE	AY485965	Triticum monococcum				
JOURNAL	AY485965	Triticum monococcum				
FEATURES	AY485965	Triticum monococcum				
source	AY485965	Triticum monococcum				
gene	AY485965	Triticum monococcum				
CDS	AY485965	Triticum monococcum				

RESULT 2	AY485966	850 bp	mrna	linear	PLN 17-MAR-2004
LOCUS	Triticum monococcum cultivar P1573529 ZCCT1 (VRN2) mRNA, complete cds.				
DEFINITION	AY485966.1 GI:45390690				
ACCESSION	AY485966				
VERSION	Triticum monococcum				
KEYWORDS	Triticum monococcum				
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.				
ORGANISM	1 (bases 1 to 850)				
REFERENCE	Yan,L., Loukianov,A., Blechl,A., Tranquilli,G., Ramakrishna,W., SanMiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J. The wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by Vernalization				
AUTHORS	Science 303 (5664), 1640-1644 (2004)				
TITLE	15016992				
JOURNAL	2 (bases 1 to 850)				
PUBMED	Yan,L., Loukianov,A., Blechl,A., Tranquilli,G., Ramakrishna,W., SanMiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J. Direct Submission				
AUTHORS	Submitted (20-NOV-2003) Agronomy and Range Science, University of California, One Shields Avenue, Davis, CA 95616, USA				
TITLE	Location/Qualifiers				
JOURNAL	1..850				
FEATURES	/organism="Triticum monococcum"				
source	/mol_type="mRNA"				
	/cultivar="P1573529"				
	/db_xref="taxon:4568"				
	/note="winter line"				
gene	1..850				
	/gene="VRN2"				
CDS	96..737				
	/gene="VRN2"				
	/note="contains CCT domain similar to Arabidopsis constant domains"				
	/codon_start=1				
	/product="ZCCT1"				
	/protein_id="AAS60238.1"				
	/db_xref="GI:45390691"				
	/translation="MSMSGCLGCANNCPRLVSPPIHHHHHHQEHQOLCEYOPFAHGNH HHHGSAADYFVPPDPDNRRTWTFREPETHAAGNSRLTLEVGAGQHWALHLYV PPARAHVFEGHAGPTNTISNAIMTIDTEMVGPAPHYPTMOERAAKVMRYRKRKR RYDKQIRYESRKAYAEALRPVNGRFVKVPEANASPSAPSPYDPSKLHLGWER"				
ORIGIN	Query Match 85.2%; Score 848.4; DB 15; Length 850; Best Local Similarity 99.9%; Pred. No. 1.7e-220; Mismatches 0; Gaps 0; Matches 849; Conservative 0				
Qy	14	TTCTTCTCGAGTCTCTCTCTCTCTCGGCTCCTCCACGACCAGACACACGAAAAAAC	73		
Db	1	TTCTTCTCGAGTCTCTCTCTCTCTCGGCTCCTCCACGACCAGACACGAAAAAAC	60		
Qy	74	AAACAAGCAAGCAAACTTGGAGCTAGCTAGCAGTAGTGCCATGTATGGGTTTGTGCG	133		
Db	61	AAACAAGCAAGCAAACTTGGAGCTAGCTAGCAGTAGTGCCATGTATGGGTTTGTGCG	120		
Qy	134	GGGCCAACCAACTCGCCGGCCCTCATGGTCTCGCCCATTCACCATCATCATCACCATCATC	193		
Db	121	GGGCCAACCAACTCGCCGGCCCTCATGGTCTCGCCCATTCACCATCATCATCACCATCATC	180		
Qy	194	AGGAGCACCAAGTGTGTGAGTACCAGTCTTCTCGCCCATTCGCAACCAACCAACCACCACC	253		
Db	181	AGGAGCACCAAGTGTGTGAGTACCAGTCTTCTCGCCCATTCGCAACCAACCAACCACCACC	240		
Qy	254	ATGGTCTGGCAGCAGACTACCAAGTGTGCCACCGCGCCGACAGAACTTCGACCCGAGAA	313		
Db	241	ATGGTCTGGCAGCAGACTACCAAGTGTGCCACCGCGCCGACAGAACTTCGACCCGAGAA	300		


```

QY 794 ATTGATCCACCGTGAAGCAGTTGTTCTCAAGTAATAAATAAGTCGGTTAGTGATGATC 853
|
|
|
Db 781 ATTGATCCACCGTGAAGCAGTTGTTCTCAAGTAATAAATAAGTCGGTTAGTGATGATC 840
|
|
|
QY 854 GATTGGAGCC 863
|
|
|
Db 841 GATTGGAGCC 850

RESULT 4
AY485967 850 bp mRNA linear PLN 17-MAR-2004
LOCUS Triticum monococcum cultivar P1221413 ZCCT1 (VRN2) mRNA, complete
DEFINITION cds.
ACCESSION AY485967
VERSION AY485967.1 GI:45390695
KEYWORDS
SOURCE Triticum monococcum
ORGANISM Triticum monococcum
REFERENCE 1 (bases 1 to 850)
AUTHORS Yan, L., Loukoianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J. L., Echenique, V. and Dubcovsky, J.
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization
JOURNAL Science 303 (5664), 1640-1644 (2004)
PUBMED 15016992
AUTHORS 2 (bases 1 to 850)
Yan, L., Loukoianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J. L., Echenique, V. and Dubcovsky, J.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA
FEATURES
source
1.850
/organism="Triticum monococcum"
/mol_type="mRNA"
/cultivar="P1221413"
/db_xref="taxon:4568"
/note="winter line"
1.850
/gene="VRN2"
96..737
/gene="VRN2"
/note="contains CCT domain similar to Arabidopsis constant
domains"
/codon_start=1
/product="ZCCT1"
/protein_id="AAS60239.1"
/db_xref="GI:45390696"
/translation="MSMSGLCGANNCPRLMSPPIHHHHHKKQLCEYQFFAHGNH
HHHHGSAADYVPVPPDPDHRRTWTFPHETAAGNSSRLTLEVGAGQMHSLVQ
PPAAHIVFPHGAFNTTISNAIMTIDTEMVGPAPHYPTMQERAAYKVMRYEKKRR
RYDKQIRYESRKAYAEIPLRVNGFRFKVPEANASPSYPSPYDPSKLHLGWR"

ORIGIN
Query Match 85.0%; Score 846.8; DB 15; Length 850;
Best Local Similarity 99.8%; Pred. No. 4,7e-220;
Matches 848; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 TTCTTCTCGAGCTCTCTCTCTCTCGGCTCTCCAGCCAGACACACACACAGAAAAAC 73
|
|
|
Db 1 TTCTTCTCGAGCTCTCTCTCTCTCGGCTCTCCAGCCAGACACACACAGAAAAAC 60
|
|
|
QY 74 AAACAGCAAGCAAACTTGGAGCTAGTAGTATGTCCATGTATCGGTTTGTGG 133
|
|
|
Db 61 AAACAGCAAGCAAACTTGGAGCTAGTAGTATGTCCATGTATCGGTTTGTGG 120
|
|
|
QY 134 GGCCAAACATGCGCGGCTCATGGTCTGGCCATTACCATCATCATCACCATCATC 193
|
|
|
Db 121 GGCCAAACATGCGCGGCTCATGGTCTGGCCATTACCATCATCATCACCATCATC 180

```

```

QY 194 AGGAGCACAGCTGTGTGAGTACAGTTCTTTCGCCCATGGCAACCAACACACACACACC 253
|
|
|
Db 181 AGAAGCACAGCTGTGTGAGTACAGTTCTTTCGCCCATGGCAACCAACACACACACACC 240
|
|
|
QY 254 ATGGCTGGGAGCAGACTTACCAGTGCACCGCCGAGCAACACTTTCGACCAACGAGCA 313
|
|
|
Db 241 ATGGCTGGGAGCAGACTTACCAGTGCACCGCCGAGCAACACTTTCGACCAACGAGCA 300
|
|
|
QY 314 CATGGACCAAGCACTTTTCATGAAACAGCAGCGGAGGAAACAGCAGCAGGCTTCAGCTGG 373
|
|
|
Db 301 CATGGACCAAGCACTTTTCATGAAACAGCAGCGGAGGAAACAGCAGCAGGCTTCAGCTGG 360
|
|
|
QY 374 AGTGGGGGCGAGGCGGCGCAACACATGGCTACCTAGTGCAGCCACCGCAGAGAGCCACA 433
|
|
|
Db 361 AGTGGGGGCGAGGCGGCGCAACACATGGCTACCTAGTGCAGCCACCGCAGAGAGCCACA 420
|
|
|
QY 434 TCGTGCCATTTTCACGGAGGTGCATTACCAACACTATTAGCAATGAAGCAATCATGACTA 493
|
|
|
Db 421 TCGTGCCATTTTCACGGAGGTGCATTACCAACACTATTAGCAATGAAGCAATCATGACTA 480
|
|
|
QY 494 TTGACACAGAGATGATGTTGGGGCTTGCCTATTATCCCAATTCGAGGAGAGAGAGCGGA 553
|
|
|
Db 481 TTGACACAGAGATGATGTTGGGGCTTGCCTATTATCCCAATTCGAGGAGAGAGAGCGGA 540
|
|
|
QY 554 AGTGTAGTATAGGAGAGAGAGAGAGAGCGGCGCTATGACAGCAAAATCCGATAGC 613
|
|
|
Db 541 AGTGTAGTATAGGAGAGAGAGAGAGAGCGGCGCTATGACAGCAAAATCCGATAGC 600
|
|
|
QY 614 AGTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGTCAACGGCGCTTTGTCAAGGTAC 673
|
|
|
Db 601 AGTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGTCAACGGCGCTTTGTCAAGGTAC 660
|
|
|
QY 674 CCGAAGCCATGGCATCGCCATCATCTCCAGCTTCGCGCTATGATCCTAGTAACTTACC 733
|
|
|
Db 661 CCGAAGCCATGGCATCGCCATCATCTCCAGCTTCGCGCTATGATCCTAGTAACTTACC 720
|
|
|
QY 734 TCGATGTTCCGGTAATTTATAGCAAGCCAGATAAAATGATTAATTTCTTCTCTG 793
|
|
|
Db 721 TCGATGTTCCGGTAATTTATAGCAAGCCAGATAAAATGATTAATTTCTTCTCTG 780
|
|
|
QY 794 ATTGATCCACCGTGAAGCAGTTGTTCTCAAGTAATAAATAAGTCGGTTAGTGATGATC 853
|
|
|
Db 781 ATTGATCCACCGTGAAGCAGTTGTTCTCAAGTAATAAATAAGTCGGTTAGTGATGATC 840
|
|
|
QY 854 GATTGGAGCC 863
|
|
|
Db 841 GATTGGAGCC 850

```

```

RESULT 5
AY485964 847 bp mRNA linear PLN 17-MAR-2004
LOCUS Triticum monococcum cultivar P1277133 ZCCT1 (VRN2) mRNA, complete
DEFINITION cds.
ACCESSION AY485964
VERSION AY485964.1 GI:45390680
KEYWORDS
SOURCE Triticum monococcum
ORGANISM Triticum monococcum
REFERENCE 1 (bases 1 to 847)
AUTHORS Yan, L., Loukoianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J. L., Echenique, V. and Dubcovsky, J.
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization
JOURNAL Science 303 (5664), 1640-1644 (2004)
PUBMED 15016992
AUTHORS 2 (bases 1 to 847)
Yan, L., Loukoianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J. L., Echenique, V. and Dubcovsky, J.

```


TITLE
JOURNAL
FEATURES
source

Direct Submission
 Submitted (20-Nov-2003) Agronomy and Range Science, University of
 California, One Shields Avenue, Davis, CA 95616, USA
 Location/Qualifiers
 1..847
 /organism="Triticum monococcum"
 /mol_type="mRNA"
 /cultivar="PI277133"
 /db_xref="taxon:4568"
 /note="winter line"
 1..847
 /gene="VRN2"
 96..734
 /gene="VRN2"
 /note="contains CCT domain similar to Arabidopsis constant
 domains"
 /codon_start=1
 /product="ZCCT1"
 /protein_id="AAS60236.1"
 /db_xref="GI:45390681"
 /translation="MSMSCGSCGANTWRPFHETAAGNSRLTLEVGAGGQMAHLVQ
 HHHGSAADVPVPPDPDHRRTTTPFETAAGNSRLTLEVGAGGQMAHLVQ
 PARAHIVPFHGGATWTSINEATMTIDENMVGPAHYPTMQERAAKVMRYREKRKR
 YDKQIRYESKAYAELEPRVRFVKVFEAWASFPSPSYDFSKULHGFWR"

ORIGIN

Query Match	83.4%;	Score 830.8;	DB 15;	Length 847;
Best Local Similarity	99.4%;	Pred. No. 1.le-215;		
Matches 845;	Conservative	0;	Mismatches 2;	Indels 3; Gaps 1;

Qy 14 TTCTTCTCGACGTCCTCTCTCTCGGCTCTCCACGCGACGACGACCAACAGAAAAAC 73
 |||||
 Db 1 TTCTTCTCGACGTCCTCTCTCTCGGCTCTCCACGCGACGACGACCAACAGAAAAAC 60
 |||||
 Qy 74 AAACAACGACGAAACCTTCGGAGCTAGCTAGCAGTATGTCCTGCTCATGCGGTTTGTGG 133
 |||||
 Db 61 AAACAACGACGAAACCTTCGGAGCTAGCTAGCAGTATGTCCTGCTCATGCGGTTTGTGG 120
 |||||
 Qy 134 GCGCCAAACAATGCGCGGCTCATGTCTCGCCATTCACCATCATCATCACCATCATC 193
 |||||
 Db 121 GCGCCAAACAATGCGCGGCTCATGTCTCGCCATTCACCATCATCATCACCATCATC 180
 |||||
 Qy 194 AGGAGCACAGCTGTGTGAGTACCAAGTTCCTTGGCCCATGGCAACCAACCAACCAACC 253
 |||||
 Db 181 AGGAGCACAGCTGTGTGAGTACCAAGTTCCTTGGCCCATGGCA--ACCACCAACCAACC 237
 |||||
 Qy 254 ATGGCTCGGACGACACTACCCAGTGCCACGCGCGCCAGACAACTTCGACACCGGAGAA 313
 |||||
 Db 238 ATGGCTCGGACGACACTACCCAGTGCCACGCGCGCCAGACAACTTCGACACCGGAGAA 297
 |||||
 Qy 314 CATGGACGACACCAATTCATGAACACGACGCGGAGGGAACAGCAGCAGGCTCACGCTGG 373
 |||||
 Db 298 CATGGACGACCAATTCATGAACACGACGCGGAGGGAACAGCAGCAGGCTCACGCTGG 357
 |||||
 Qy 374 AGGTGGCGCAGCGCGGCAACACATGGCTCACCTAGTGCACCCAGCCAGGAGGCCACA 433
 |||||
 Db 358 AGGTGGCGCAGCGCGGCAACACATGGCTCACCTAGTGCACCCAGCCAGGAGGCCACA 417
 |||||
 Qy 434 TCGTGCCATTTACGGAGGTGCATTACCAACACTATTAGCAATGAAGCAATCATGACTA 493
 |||||
 Db 418 TCGTGCCATTTACGGAGGTGCATTACCAACACTATTAGCAATGAAGCAATCATGACTA 477
 |||||
 Qy 494 TTGACACAGAGATGATGGTGGGGCTCCGCCATTATCCCAATGCAAGGAGAGACGACGA 553
 |||||
 Db 478 TTGACACAGAGAATGATGGTGGGGCTCCGCCATTATCCCAATGCAAGGAGAGACGACGA 537
 |||||
 Qy 554 AGGTGATGAGGTATAGGAGAGAGGAGGCGGCGCTTATGACAAGCAAAATCCGATACG 613
 |||||
 Db 538 AGGTGATGAGGTATAGGAGAGAGGAGGCGGCGCTTATGACAAGCAAAATCCGATACG 597
 |||||
 Qy 614 AGTCCAGAAAGCTTACGCTGAGCTTCGGGCAATGGGTCAAACGCGCGCTTTGTCAAGGTAC 673
 |||||
 Db 598 AGTCCAGAAAGCTTACGCTGAGCTTCGGGCAAGGGTCAACGCGCGCTTTGTCAAGGTAC 657
 |||||

Db 171 CGCGGACTACCCACGCCACCGCCACCGTGGCCCAATTCGCCACCACTGCAGATCATGGA 230
QY 320 CCAGACCATTTTCATGAACACGACGCGGACGAGGACGACGAGGCTCACGCTGGAGGTGG 379
Db 231 CCACACCGTTTCATGAACACGACGCTGCAGGGAACAGCAGCACTCACGCTGGAGGTAG 290
QY 380 GCGCAGCGCGCCACACATGGCTCAGCTAGTACGAGCCACCGG-----CAAGAGCCACA 433
Db 291 ATCAGCGCGCGCCAAACATGGCTCAGCTGCTGAGCGCCACCGGCGCCCAAGAACACCA 350
QY 434 TCGTGCATTTACGCGAGGTGCATTCACCAACACTATTAGCAATGAAGCAATCATCACTA 493
Db 351 TCGTGCATTTCTCGGGGCTGCATTCACAGCACTATTAGCAATGAAGCAATCATCACTA 410
QY 494 TTGACACAGATGATGGTGGGCGCTGCCCATTTATCCCAATTCACAGGAGAGAGCGGA 553
Db 411 TTGATACAGATGATGGTGGGCGCTGCCCATTTATCCCAATTCACAGGAGAGAGCGGA 470
QY 554 AGGTGATAGGTATAGGAG 613
Db 471 AGGTGATAGGTATAGGAG 530
QY 614 AGTCCAGAAAAGCTTACGCTGAGCTTCCGCGCATTCGCGCTCAACGCGCTTTGTCAAGGTAC 673
Db 531 AGTCCAGAAAAGCTTACGCGAGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
QY 674 CCGAGCCATGGCATCGCCATCATTCACGCTTCCGCGCTTATGATCCTAGTAACTTCACC 733
Db 591 CAGAGCCGCTGCATCGTCAACCCCGAGCTTCCGCGCTTATGATCCTAGTAACTTCACC 650
QY 734 TCGGATGGTTCGGTAAATTTATAGCAACAGCCAGCAAGCAATTAATATACATATT 785
Db 651 TCGGATGGTTCAGTAGTATTTTTCATCAAAAGTAAATTAAGTTGGTTATTGATT 702

RESULT 10
AY485976

LOCUS Triticum monococcum cultivar P1272561 ZCCT2 (VRN2) mRNA linear PLN 17-MAR-2004
DEFINITION cds.

ACCESSION AY485976

VERSION AY485976.1 GI:45390733

KEYWORDS

SOURCE Triticum monococcum

ORGANISM

Triticum monococcum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 712)

Yan, L., Loukianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J. L., Echenique, V. and Dubcovsky, J.

The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by

Vernalization

Science 303 (5664), 1640-1644 (2004)

JOURNAL PUBMED 15016992

REFERENCE 2 (bases 1 to 712)

Yan, L., Loukianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J. L., Echenique, V. and Dubcovsky, J.

Direct Submission

Submitted (20-NOV-2003) Agronomy and Range Science, University of

California, One Shields Avenue, Davis, CA 95616, USA

Location/Qualifiers

1. .712

/organism="Triticum monococcum"

/mol_type="mRNA"

/cultivar="P1272561"

/db_xref="taxon:4568"

/note="winter line"

1. .712

/gene="VRN2"

29. .667

/gene="VRN2"

gene

CDS

/note="contains CCT domain similar to Arabidopsis constant
domains"
/codon_start=1
/product="ZCCT2"
/protein_id="AAS60248.1"
/db_xref="GI:45390733"
/translation="MSMSGCLGASDCPHMISPLVQHQBHWLREYQFTQGHHHHH
HGAADYPPPPPPSANCHRSWTFPHETAAGNSRLTLEVDAGGNMHLLOPPA
RPRTIVPFCGAFTSTINATITDEMVMGAHNLTQREAKVRYRKRKRC
YDKQIRYSRKAYAELEPRVNGCFVKVPEAAASSPPASPDYPSKHLGWFO"

ORIGIN

Query Match 46.6%; Score 464.4; DB 15; Length 712;
Best Local Similarity 81.5%; Pred. No. 1.8e-115;
Matches 580; Conservative 0; Mismatches 116; Indels 16; Gaps 3;
QY 80 GCAAGCAAAACCTTGAGAGCTAGCTAGCAGTATGTCATGTCTCATGTCTGCGGGCGCA 139
Db 1 GCATCAAAACGTAGGGGCTAGCT-GCAGTATGTCATGTCTCATGTCTGCGGGCGCA 59
QY 140 ACAACTGCCCGCGCTCATGTCTCGCCCATTTCAACCATCATCATCAATCATCAGGAGC 199
Db 60 GCGACTGCCCGCACCATGATCTCGCCGT-----TCTTCAGCATCAGGAACAAC 110
QY 200 ACCAGCTGTGTAGTACAGTCTTTCGCCCATTCGCAACCAACCAACCAACCAACCATGGCT 259
Db 111 ACTGGCTGCGGAGTACCAAGTCTTTCACCAAGGCCACCAACCAACCAACCAACCGCGG 170
QY 260 CGGAGCAGAGATACCCAGTCCGCGCCGCGCAGCAAACTTCGACCAACCGCAACATGGA 319
Db 171 CGGCGACTACCCAGCGCCACCGCCAGTCTGCGCCATTCGCCCATTCGCAATCATGGA 230
QY 320 CCAGACCATTTTCATGAACACGAGCGGCGGAGAAACAGCAGAGGCTCAAGTGGAGGTGG 379
Db 231 CCACACCGTTTCATGAACACGAGCTGCAGGAGAAACAGCAGCAGAGCTCAAGTGGAGGTAG 290
QY 380 GCGAGGCGGCGCAACACATGCTCAGTGTGCGAGCCACCGG-----CAAGAGCCACA 433
Db 291 ATGACGCGGCGCAAAACATGCTCAGTGTGCGAGCCACCGGCGCAGGCGCAAGAACCA 350
QY 434 TCGTGCATTTTCAGGAGGTGCATTCACCAACACTATTAGCAATGAAGCAATCATCACTA 493
Db 351 TCGTGCATTTTCGCGGCGCTGCATTCACAGCACTATTAGCAATGAAGCAATCATCACTA 410
QY 494 TTGACACAGATGATGTGGGGCTGCCCATTTATCCCAATTCAGGAGAGAGAGAGCGGA 553
Db 411 TTGATACAGATGATGTGGGGCTGCCCATTTATCTCAGCATGCAGGAGAGAGAGCGGA 470
QY 554 AGGTGATAGGTATAGGAGAGAGAGAGAGAGCGGCGCTATGCAAGCAATTCGATAGC 613
Db 471 AGGTGATAGGTATAGGAGAGAGAGAGAGAGCGGCGTGTCTATGCAAGCAATTCGCTAGC 530
QY 614 AGTCCAGAAAAGCTTACGCTGAGCTTCCGCGCATTCGCGCTCAACGCGCTTTGTCAAGGTAC 673
Db 531 AGTCCAGAAAAGCTTACGCGAGTACAGGAGAGAGAGAGAGCGGCTCAATGGCTGCTTTGTCAAGGTAC 590
QY 674 CCGAGCCATGGCATCGCCATCATTCACGCTTCCGCGCTTATGATCCTAGTAACTTCACC 733
Db 591 CAGAGCCGCTGCATCGTCAACCCCGAGCTTCCGCGCTTATGATCCTAGTAACTTCACC 650
QY 734 TCGGATGGTTCGGTAAATTTATAGCAACAGCCAGCAAGCAATTAATATACATATT 785
Db 651 TCGGATGGTTCAGTAGTATTTTTCATCAAAAGTAAATTAAGTTGGTTATTGATT 702

RESULT 11

AY485979

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

AY485979 2078 bp DNA linear PLN 17-MAR-2004
Triticum turgidum cultivar Langdon ZCCT1-Td (VRN2) gene, complete
cds.
AY485979
AY485979.1 GI:45390744

SOURCE Triticum turgidum
ORGANISM Triticum turgidum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 2078)
AUTHORS Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization
JOURNAL Science 303 (5664), 1640-1644 (2004)
PUBMED 15016992
REFERENCE 2 (bases 1 to 2078)
AUTHORS Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA
FEATURES
source
1..2078
/organism="Triticum turgidum"
/mol_type="genomic DNA"
/cultivar="Langdon"
/db_xref="taxon:4571"
/clone="BAC 354M17"
/note="winter line; tetraploid genome A"
<96..>1965
/gene="VRN2"
join(96..401,1651..>1965)
/gene="VRN2"
/product="ZCCT1-Td"
join(96..401,1651..1965)
/gene="VRN2"
/codon_start=1
/product="ZCCT1-Td"
/protein_id="AAS60251.1"
/db_xref="GI:45390745"
/translation="MSMSGCLGANNCPRLMVSPPIHRRHHHQBHLQHOFFAQQNH
HHHPVLPFPNDSRHTWTFPHETAAGNSRUTLEVGAGRPMAHLVOPPARAHI
VPFYGATFTINSAINITIDTMVGPATPTMOERAARKVMRYEKRRYDKQIR
YESKAYAEALRPVNGCFVKVPEANASPSASPYPDSKLHLGWER"
ORIGIN
Query Match 42.2%; Score 420; DB 15; Length 2078;
Best Local Similarity 98.8%; Pred. No. 3e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 423; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 436 GTGCCATTTACGAGGTCATTACCAACACTATTAGCAATGAAGCAATCATGACTATT 495
DB 1651 GTGCCATTTACGAGGTCATTACCAACACTATTAGCAATGAAGCAATCATGACTATT 1710
QY 496 GACACAGAGATGATGGGGCTGCCCATTTATCCCAATGCAGGAGAGACGCGAAG 555
DB 1711 GACACAGAGATGATGGGGCTGCCCATTTATCCCAATGCAGGAGAGACGCGAAG 1770
QY 556 GTGATGAGGTA TAGGAGAGAGAGAGCGCGCTATGACAAATCCGATACGAG 615
DB 1771 GTGATGAGGTA TAGGAGAGAGAGAGCGCGCTATGACAAATCCGATACGAG 1830
QY 616 TCCAGAAAGCTTACGCTGAGCTTCGGCCATCGGTCACGCGCGCTTTGTCAAGGTACCC 675
DB 1831 TCCAGAAAGCTTACGCTGAGCTTCGGCCATCGGTCACGCGCGCTTTGTCAAGGTACCC 1890
QY 676 GAAGCCATGGCATCGCCATCATCTCCAGCTTCGCCCTATGATCTAGTAAACTTCCACCTC 735
DB 1891 GAAGCCATGGCTCGCCATCATCTCCAGCTTCGCCCTATGATCTAGTAAACTTCCACCTC 1950
QY 736 GGATGGTTCGGTAATTTATGACAAAGCCAGATAAATGATAAATATTTCTCTGAT 795
DB 1951 GGATGGTTCGGTAATTTATGACAAAGCCAGATAAATGATAAATATTTCTCTGAT 2010
QY 796 TGATCCACCGTGAGCAGTGTCTTCTCAAGTAAATGAAGTCGGTTAGTATGATCGA 855

DB 2011 TGATCCACCGTGAGCAGTGTCTTCTCAAGTAAATGAAGTCGGTTAGTATGATCGA 2070
QY 856 TTGAGGCC 863
DB 2071 TTGAGGCC 2078
RESULT 12
AY485644_2/c
WPCOMMENT
Sequence split into 5 fragments LOCUS AY485644 Accession AY485644
Fragment Name Begin End
AY485644_0 1 110000
AY485644_1 100001 210000
AY485644_2 200001 310000
AY485644_3 300001 410000
AY485644_4 400001 438828
Continuation (3 of 5) of AY485644 from base 200001 (AY485644 Triticum monococcum phospho-
putative transposase, phosphatidylinositol phospho...
Query Match 32.2%; Score 320.8; DB 15; Length 110000;
Best Local Similarity 77.4%; Pred. No. 9e-76; Mismatches 62; Indels 64; Gaps 1;
Matches 432; Conservative 0; Mismatches 0; Mismatches 62; Indels 64; Gaps 1;
QY 436 GTGCCATTTACGAGGTCATTACCAACACTATTAGCAATGAAGCAATCATGACTATT 495
DB 54220 GTGCCATTTCTCGGGGCTGCAATTCACGAGCACTATTAGCAATGAAGCAATCATGACTATT 54161
QY 496 GACACAGAGATGATGGGGCTGCCCATTTATCCCAATGCAGGAGAGACGCGAAG 555
DB 54160 GACACAGAGATGATGGGGGCTGCCCATTAATCTGACGATGCAGGAGAGACGCGAAG 54101
QY 556 GTGATGAGGTA TAGGAGAGAGAGAGCGCGCTATGACAAATCCGATACGAG 615
DB 54100 GTGATGAGGTA TAGGAGAGAGAGAGCGCGCTATGACAAATCCGCTACGAG 54041
QY 616 TCCAGAAAGCTTACGCTGAGCTTCGGCCATCGGTCACGCGCGCTTTGTCAAGGTACCC 675
DB 54040 TCCAGAAAGCTTACGCGAGCTCAGGCCACGGGTCAATGGCTGCTTTGTCAAGGTACCA 53981
QY 676 GAAGCCATGGCATCGCCATCATCTCCAGCTTCGCCCTATGATCTAGTAAACTTCCACCTC 735
DB 53980 GAAGCGCTGATCGCTGCTACCCCGCTTCAGCTATGATCTAGTAAACTTCCACCTC 53921
QY 736 GGATGGTTCGGTAATTTATGACAAAGCCAGATAAATGATAAATATTTCTCTGAT 795
DB 53920 GGATGGTTCAGTAGTATT----- 53903
QY 796 TGATCCACCGTGAGCAGTGTCTTCTCAAGTAAATGAAGTCGGTTAGTATGATCGA 855
DB 53902 -----TTCAATCAAGTAAATGAAGTTGGTTATTGATGACCGA 53865
QY 856 TTGAGCCATTTATGTTGACTTTGACTATTATAAATGGTCAGCAGATCAATCAACAAAATG 915
DB 53864 CGGAGGAGTATTGTTGATTGACTATTTCAAAAGTCAGCAAAACCAATCAAGAAAATG 53805
QY 916 TATTTATGAAACAAGCTTCTGTATATACGCTGTTGATTTAAACATGTAAATTTCAAGAGG 975
DB 53804 TATTTGTTGAAACAAGTATTCTTATGCTTTATGTTAATTTAAGCATGTAATTTGAGGAGG 53745
QY 976 ATAGCTACTTTGATGCTGT 993
DB 53744 CTAGCTACTTAGATGTGT 53727
RESULT 13
AY485980
LOCUS AY485980 1790 bp DNA linear PLN 17-MAR-2004
DEFINITION Triticum turgidum cultivar Langdon ZCCT2-Td (VRN2) gene, complete
cds.
ACCESSION AY485980
VERSION AY485980.1 GI:45390748
KEYWORDS

```

SOURCE      Triticum turgidum
ORGANISM    Triticum turgidum
DEFINITION  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Poideae; Triticeae; Triticum.
REFERENCE   1 (bases 1 to 1790)
AUTHORS    Yan,L., Loukolanov,A., Blechl,A., Tranquilli,G., Ramakrishna,W.,
              SanMiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J.
TITLE      The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
              Vernalization
JOURNAL     Science 303 (5664), 1640-1644 (2004)
PUBMED     15016992
REFERENCE   2 (bases 1 to 1790)
AUTHORS    Yan,L., Loukolanov,A., Blechl,A., Tranquilli,G., Ramakrishna,W.,
              SanMiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J.
TITLE      Direct Submission
JOURNAL     Submitted (20-NOV-2003) Agronomy and Range Science, University of
              California, One Shields Avenue, Davis, CA 95616, USA
FEATURES   source
            1..1790
            /organism="Triticum turgidum"
            /mol_type="genomic DNA"
            /cultivar="lanadon"
            /db_xref="taxon:4571"
            /clone="BAC 32682"
            /note="winter line; tetraploid genome A"
            <29..>1745
            /gene="VRN2"
            join(<29..352,1431..>1745)
            /gene="VRN2"
            /product="ZCCT2-Td"
            join(29..352,1431..1745)
            /gene="VRN2"
            /codon_start=1
            /product="ZCCT2-Td"
            /protein_id="AAS60252.1"
            /db_xref="GI:45390749"
            /translation="MPMSGLCGASDCPHMTSPVLOHQHRLREYFFFTGGHHHH
              HDAAADYPPPPSANCHECHRSWTFPHETAAGNSRLTLEVDAGGONMAHLLQPPA
              RPTTIVPCGAFTSTISNATIMTIDTMVGAHNTMOEREAKVMRYREKRKR
              YDKQIRYESRKAYAELEPRVNGRFVKVPEAAASSPPSPDPSKLHLGWF"

ORIGIN
Query Match      26.8%; Score 267.2; DB 15; Length 1790;
Best Local Similarity 86.0%; Pred. No. 1.8e-61;
Matches 296; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

QY 436 GTGCCATTTCAGGAGTGCTATCCACCAACTATTAGCAATGAAGCAATCATGACTATT 495
DB 1431 GTGCCATTTCGGGGCTGCATTCCACGACTATTAGCAATGAAGCAATCATGACTATT 1490
QY 496 GACACAGATCATGTGGGGCTGCCCATTTCCACAAATGCAGAGAGACGCGAAG 555
DB 1491 GATACAGATCATGTGGGGCTGCCCATTTCTGACGATGAGGAGAGAGGCGAAG 1550
QY 556 GTGATGAGGTATAGGAGAGAGAGAGAGGCGCGCTATGACAAGCAAAATCCGATACGAG 615
DB 1551 GTGATGAGGTATAGGAGAGAGAGAGAGGCGCGTGTATGACAAGCAAAATCCGATGAG 1610
QY 616 TCCAGAAAGCTTACGCTAGCTTCGGCCATGGGTCAACGGCGCTTTGTCAAGTACCC 675
DB 1611 TCCAGAAAGCTTACGCTAGCTTCAGCGAGTTCAGCGCCAGCGGTCAATGGCGCTTTGTCAAGTACCA 1670
QY 676 GAAGCCATGGCATCGGCATCATCTCCAGCTTCGCCCTATGATCCCTAGTAACTTCACTTC 735
DB 1671 GAAGCCGCTGCATCGTGTGTACCCCGAGCTTGGCCCTATGATCCCTAGTAACTTCACTTC 1730
QY 736 GGATGGTTCGGTAAATTTATAGCACAAGCCAGATATAAATGATAA 779
DB 1731 GGATGGTTCGGTAAATTTTTCATCAAGTAAATTAAGTTGGTTA 1774

RESULT 14

```

```

AY485978    2064 bp      DNA      linear      PLN 17-MAR-2004
LOCUS       Hordeum vulgare cultivar Dairokkaku ZCCT-Hb (VRN2) gene, partial
DEFINITION  cds.
ACCESSION   AY485978
VERSION     AY485978.1 GI:45390740
KEYWORDS    Hordeum vulgare
SOURCE      Hordeum vulgare
ORGANISM    Hordeum vulgare
DEFINITION  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Poideae; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 2064)
AUTHORS    Yan,L., Loukolanov,A., Blechl,A., Tranquilli,G., Ramakrishna,W.,
              SanMiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J.
TITLE      The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
              Vernalization
JOURNAL     Science 303 (5664), 1640-1644 (2004)
PUBMED     15016992
REFERENCE   2 (bases 1 to 2064)
AUTHORS    Yan,L., Loukolanov,A., Blechl,A., Tranquilli,G., Ramakrishna,W.,
              SanMiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J.
TITLE      Direct Submission
JOURNAL     Submitted (20-NOV-2003) Agronomy and Range Science, University of
              California, One Shields Avenue, Davis, CA 95616, USA
FEATURES   source
            1..2064
            /organism="Hordeum vulgare"
            /mol_type="genomic DNA"
            /cultivar="Dairokkaku"
            /db_xref="taxon:4513"
            /note="winter barley"
            <420..>2064
            /gene="VRN2"
            join(<420..752,1756..>2064)
            /gene="VRN2"
            /product="ZCCT-Hb"
            join(420..752,1756..>2064)
            /gene="VRN2"
            /protein_id="AAS60250.1"
            /db_xref="GI:45390741"
            /translation="MSMAGLCGASNCYPHMSVLLHHHHQHQREYQFPAQHGH
              HHHGAAADYPPPPANCHRRSWATLFHETAPVNSTLTQSDVAGGQMAHLLQ
              PPAPRATVPFRSAFTTISNATIMTIDTMVGAHNTMOEREAKVMRYREKRKR
              KRYDKQIRYESRKAYAELEPRVNGRFVKVPEAAASSPPSPDPSSELHLGWF"

ORIGIN
Query Match      25.2%; Score 251.4; DB 15; Length 2064;
Best Local Similarity 88.3%; Pred. No. 4e-57;
Matches 273; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 436 GTGCCATTTCAGGAGTGCTATCCACCAACTATTAGCAATGAAGCAATCATGACTATT 495
DB 1756 GTGCCATTTCGGCGAGTGCTATCCACCAACTATTAGCAATGAAGCAATCATGACTATT 1815
QY 496 GACACAGATCATGTGGGGCTGCCCATTTCCACAATGCAGAGAGACGCGAAG 555
DB 1816 GATACAGATCATGTGGGGCTGCCCATTTAGTCCAACGATGAGGAGAGAGCAAG 1875
QY 556 GTGATGAGGTATAGGAGAGAGAGAGAGGCGCGCTATGACAAGCAAAATCCGATACGAG 615
DB 1876 GTGATGAGGTATAGGAGAGAGAGAGAGGCGCGCTATGACAAGCAAAATCCGATACGAG 1935
QY 616 TCCAGAAAGCTTACGCTAGCTTCGGCCATGGGTCAACGGCGCTTTGTCAAGTACCC 675
DB 1936 TCCAGAAAGCTTACGCTAGCTTAGGCCACGGGTCAACGGCGCTTTGTCAAGTACCT 1995
QY 676 GAAGCCATGGCATCGGCATCATCTCCAGCTTCGCCCTATGATCCCTAGTAACTTCACTTC 735
DB 1996 GAAGCCGCTGGTCAACCATACCCCGAGCTTCGCCCGCATGATCCTAGTCACTTCACTTC 2055

```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 11:51:16 : Search time 714 Seconds

(without alignments)
9296.986 Million cell updates/sec

Title: US-10-723-947-75

Perfect score: 996

Sequence: 1 taactgcctctctcttcc.....tagctacttgatgtgtaat 996

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 21.*

1: Geneseqn1980s.*

2: Geneseqn1990s.*

3: Geneseqn2000s.*

4: Geneseqn2001as.*

5: Geneseqn2001bs.*

6: Geneseqn2002as.*

7: Geneseqn2002bs.*

8: Geneseqn2003as.*

9: Geneseqn2003bs.*

10: Geneseqn2003cs.*

11: Geneseqn2003ds.*

12: Geneseqn2004as.*

13: Geneseqn2004bs.*

14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	996	100.0	996	ADs19577	ADs19577 One grain
2	907.2	91.1	375	ADs19581	ADs19581 Langdon (
3	561	56.3	7051	ADs19576	ADs19576 One grain
4	553	55.5	2913	ADs19580	ADs19580 Langdon (
5	455.2	45.7	642	ADs19593	ADs19593 Winter ba
6	451.4	45.3	639	ADs19587	ADs19587 Langdon (
7	449	45.1	639	ADs19590	ADs19590 Winter ba
8	445	44.7	639	ADs19584	ADs19584 One grain
9	320.8	32.2	3454	ADs19586	ADs19586 Langdon (
10	320.8	32.2	5734	ADs19583	ADs19583 One grain
11	251.4	25.2	2043	ADs19592	ADs19592 Winter ba
12	247.6	24.9	1985	ADs19589	ADs19589 Winter ba
13	93	9.3	1078	ADs16780	ADs16780 Lhd4-rela
14	93	9.3	1078	ADs16786	ADs16786 Lhd4-rela
15	93	9.3	1078	ADs16783	ADs16783 Lhd4-rela
16	93	9.3	2723	ADs16785	ADs16785 Lhd4-rela
17	93	9.3	2723	ADs16779	ADs16779 Lhd4-rela
18	93	9.3	2723	ADs16782	ADs16782 Lhd4-rela
19	76.6	7.7	385	ABZ12460	ABZ12460 Arabidops

20	76.6	7.7	1075	13	ADx47666	Adx47666 Plant ful
21	76.6	7.7	1120	12	ADO02184	ADO02184 Thalecres
22	76.6	7.7	1125	3	AAC47873	AAC47873 Arabidops
23	76.6	7.7	1127	3	AAC45341	AAC45341 Arabidops
24	76.6	7.7	1141	10	ADB31874	ADB31874 DNA encod
25	75.4	7.6	577	12	ADJ39390	ADJ39390 Plant CDN
26	74.8	7.5	1002	12	ADJ39403	ADJ39403 Plant CDN
27	74.6	7.5	1388	14	AEb65256	AEb65256 Rice geno
28	73.6	7.4	1461	13	ADx32661	ADx32661 Plant ful
29	73.2	7.3	623	3	AAx78441	AAx78441 Plant SDF
30	72.2	7.2	388	10	ADK54130	ADK54130 Plant DNA
31	71.8	7.2	1068	12	ADN72948	ADN72948 Thale cre
32	71.8	7.2	1297	6	ABN98249	ABN98249 Arabidops
33	71.8	7.2	1370	13	ADx31777	ADx31777 Plant ful
34	71.8	7.2	1374	3	AAC46126	AAC46126 Arabidops
35	71.8	7.2	1377	3	AAC32926	AAC32926 Arabidops
36	71.8	7.2	1404	13	ADx30238	ADx30238 Plant ful
37	70	7.0	734	9	ADA49038	ADA49038 Wheat gen
38	70	7.0	734	10	ADC03443	ADC03443 Wheat flo
39	70	7.0	734	11	ACL32613	ACL32613 Rice abio
40	70	7.0	1132	13	ADx50712	ADx50712 Plant ful
41	70	7.0	1229	13	ADx47569	ADx47569 Plant ful
42	69.4	7.0	596	13	ACN60093	ACN60093 Cotton gy
43	68.4	6.9	533	13	ACN61587	ACN61587 Cotton gy
44	65.2	6.6	1728	14	ADM16414	ADM16414 E Grandis
45	65.8	6.6	699	9	ADA48119	ADA48119 Rice gene

ALIGNMENTS

RESULT 1

ADs19577
ID ADs19577 standard; cDNA; 996 BP.

XX ADs19577;

XX 30-DEC-2004 (first entry)

DE One grained wheat DV92 ZCCT1 cDNA.

XX One grained wheat; chromosome 5a; ss; APETALAL1; API; vernalisation;
KW flowering; ZCCT1; ZCCT2; vrnl1; vrnl2; CARG box; plant; gene.

XX Triticum monococcum.

XX US2004205848-A1.

XX 14-OCT-2004.

XX 26-NOV-2003; 2003US-00723947.

XX 11-APR-2003; 2003US-00412137.

XX (REGC) UNIV CALIFORNIA.

XX Dubcovsky J, Yan L, Loukoianov A;

XX WPI; 2004-728059/71.

XX P-PSDB; ADS19578.

XX New recombinant ZCCT1 protein coding sequence useful for altering a
FT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.

XX Claim 1; SEQ ID NO 75; 115pp; English.

XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
CC domain protein) coding sequence comprising a nucleic acid that hybridizes
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
CC the identification of to genes, vrnl1 identified as API (APETALAL1) and
CC vrnl2 identified as ZCCT1 controlling vernalisation of flowering in
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes

QY 496 GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATCCAGAGAGACGCGAAG 555
DB 4642 GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATCCAGAGAGACGCGAAG 4701
QY 556 GTGATGAGTATAGGAG 615
DB 4702 GTGATGAGTATAGGAG 4761
QY 616 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATCGGCTCAACGGCGCTTTGTCAAGGTACCC 675
DB 4762 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATCGGCTCAACGGCGCTTTGTCAAGGTACCC 4821
QY 676 GAAGCCATGGCATCGCATCATCTCCAGCTTCGGCCATCGATCCCTATGATCCCTCAACCTC 735
DB 4822 GAAGCCATGGCATCGCATCATCTCCAGCTTCGGCCATCGATCCCTATGATCCCTCAACCTC 4881
QY 736 GGATGGTCCGGTAATTTATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 795
DB 4882 GGATGGTCCGGTAATTTATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4941
QY 796 TGATCCACCCCGTGAAGCAGTGTCTCTCAAGTAAATTAAGTCGGTTAGTGATTCGATCGA 855
DB 4942 TGATCCACCCCGTGAAGCAGTGTCTCTCAAGTAAATTAAGTCGGTTAGTGATTCGATCGA 5001
QY 856 TTGGAGCCATTAATGTTGACTTGACTTATTAATAATGGTCAGAGATCAATCAACAAAATG 915
DB 5002 TTGGAGCCATTAATGTTGACTTGACTTATTAATAATGGTCAGAGATCAATCAACAAAATG 5061
QY 916 TATTTATTGAACAAGTCTTGTTATCTAGTACGTTGATTTAAACATGTAATTTCAAGAGG 975
DB 5062 TATTTATTGAACAAGTCTTGTTATCTAGTACGTTGATTTAAACATGTAATTTCAAGAGG 5121
QY 976 ATAGTACTTTTGATGTGAAT 996
DB 5122 ATAGTACTTTTGATGTGAAT 5142

RESULT 4

ADSL19580
ID ADSL19580 standard; DNA; 2913 BP.
XX
AC ADSL19580;
XX
DT 30-DEC-2004 (first entry)
XX
DE Langdon (tetraploid) wheat ZCCT1 genomic DNA.
XX
KW Wild emmer wheat; ds; APETALA1; AP1; vernalisation; flowering; ZCCT1;
KW ZCCT2; vrn1; vrn2; CARG box; plant; gene.
XX
OS Triticum turgidum; subsp. dicoccoides.
XX
FN US2004205848-A1.
XX
PD 14-OCT-2004.
XX
PF 26-NOV-2003; 2003US-00723947.
XX
PR 11-APR-2003; 2003US-00412137.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Dubcovsky J, Yan L, Loukolanov A;
XX
DR WPI; 2004-728059/71.
DR P-FSDB; ADS19582.
XX
PT New recombinant ZCCT1 protein coding sequence useful for altering a
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.
XX
PS Disclosure; SEQ ID NO 78; 115pp; English.
XX

CC The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
CC domain protein) coding sequence comprising a nucleic acid that hybridises
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
CC the identification of to genes, vrn1 identified as AP1 (APETALA1) and
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
CC have been localised to chromosome 5a of one grained wheat, triticum
CC monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a
CC binding site for ZCCT1 termed the CARG box. Also included are a vector
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell
CC comprising the vector, a transgenic plant comprising the recombinant
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits
CC ZCCT1 repression of AP1), a seed from the transgenic plant, a method for
CC altering a plant's response to vernalisation and a molecular marker for
CC vrn2 derived from ADS19577. The genetic construct is an interference RNA
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
CC a repressor defective ZCCT1 protein operably linked to a promoter or a
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
CC operably linked to a promoter. The present sequence is a plant ZCCT
CC genomic DNA sequence.
XX

Seq Sequence 2913 BP; 867 A; 627 C; 575 G; 844 T; 0 U; 0 Other;

Query Match 55.5%; Score 553; DB 13; Length 2913;
Best Local Similarity 99.1%; Pred. No. 1.2e-154;
Matches 556; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 436 GTGCCATTTTCCAGGAGGTGCATTCCACCAACTATTAGCAATGAAGCAATCATGACTATT 495
DB 2133 GTGCCATTTTCCAGGAGGTGCATTCCACCAACTATTAGCAATGAAGCAATCATGACTATT 2192
QY 496 GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATGCGAGAGAGACGCGAAG 555
DB 2193 GACACAGAGATGATGGTGGGGCTGCCCATTTATCCCAATGCGAGAGAGACGCGAAG 2252
QY 556 GTGATGAGTATAGGAG 615
DB 2253 GTGATGAGTATAGGAG 2312
QY 616 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATCGGCTCAACGGCGCTTTGTCAAGGTACCC 675
DB 2313 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATCGGCTCAACGGCGCTTTGTCAAGGTACCC 2372
QY 676 GAAGCCATGGCATCGCCATCATCTCCAGCTTCGGCCATCGATCCCTATGATCCCTC 735
DB 2373 GAAGCCATGGCATCGCCATCATCTCCAGCTTCGGCCATCGATCCCTATGATCCCTC 2432
QY 736 GGATGGTCCGGTAATTTATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 795
DB 2433 GGATGGTCCGGTAATTTATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2492
QY 796 TGATCCACCCCGTGAAGCAGTGTCTCTCAAGTAAATTAAGTCGGTTAGTGATTCGATCGA 855
DB 2493 TGATCCACCCCGTGAAGCAGTGTCTCTCAAGTAAATTAAGTCGGTTAGTGATTCGATCGA 2552
QY 856 TTGGAGCCATTAATGTTGACTTGACTTATTAATAATGGTCAGAGATCAATCAACAAAATG 915
DB 2553 TTGGAGCCATTAATGTTGACTTGACTTATTAATAATGGTCAGAGATCAATCAACAAAATG 2612
QY 916 TATTTATTGAACAAGTCTTGTTATCTAGTACGTTGATTTAAACATGTAATTTCAAGAGG 975
DB 2613 TATTTATTGAACAAGTCTTGTTATCTAGTACGTTGATTTAAACATGTAATTTCAAGAGG 2672
QY 976 ATAGTACTTTTGATGTGAAT 996
DB 2673 ATAGTACTTTTGATGTGAAT 2693

RESULT 5

ADSL19593
ID ADSL19593 standard; cDNA; 642 BP.
XX

temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes have been localised to chromosome 5a of one grained wheat, Triticum monococcum. ZCCT1 is the repressor of APl whose promoter contains a binding site for ZCCT1 termed the CARG box. Also included are a vector comprising the recombinant ZCCT1 protein coding sequence above, a cell comprising the vector, a transgenic plant comprising the recombinant ZCCT1 protein coding sequence above (or a genetic construct that inhibits ZCCT1 repression of APl), a seed from the transgenic plant, a method for altering a plant's response to vernalisation and a molecular marker for vrn2 derived from AUS19577. The genetic construct is an interference RNA construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding a repression defective ZCCT1 protein operably linked to a promoter or a nucleic acid sequence encoding a DNA binding defective ZCCT1 protein operably linked to a promoter. The present sequence is a plant ZCCT cDNA sequence.

SQ Sequence 639 BP; 161 A; 200 C; 172 G; 106 T; 0 U; 0 Other;

Query Match	45.3%	Score 451.4;	DB 13;	Length 639;
Best Local Similarity	83.6%	Pred. NO. 1.6e-124;		
Matches 541;	Conservative 0;	Mismatches 91;	Indels 15;	Gaps 2;

[illegible]

RESULT 7
ADSL9590
ID ADSL9590 standard; CDNA; 639 BP.
XX
AC ADSL9590;

XX	30-DEC-2004 (first entry)	
DT		
XX		
DE	Winter barley ZCCT-Ha CDNA.	
XX		
KW	Barley; ss; APETALA1; APL; vernalisation; flowering; ZCCT1; ZCCT2; vrn1;	
KW	vrn2; CARG box; plant; gene.	
XX		
OS	Hordeum vulgare.	
XX		
PN	US2004205848-A1.	
XX		
PD	14-OCT-2004.	
XX		
PF	26-NOV-2003; 2003US-00723947.	
XX		
PR	11-APR-2003; 2003US-00412137.	
XX		
PA	(REGC) UNIV CALIFORNIA.	
XX		
PI	Dubcovsky J, Yan L, Loukoianov A;	
XX		
DR	WPI; 2004-728059/71.	
XX	P-PSDB; ADS19591.	
XX		
PT	New recombinant ZCCT1 protein coding sequence useful for altering a	
PT	plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to	
PT	vernalization or flowering times.	
XX		
PS	Disclosure; SEQ ID NO 88; 115pp; English.	

The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT domain protein) coding sequence comprising a nucleic acid that hybridises to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses the identification of genes, vrn1 identified as AP1 (APEXALAI) and vrn2 identified as ZCCT1 controlling vernalisation of flowering in temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes have been localised to chromosome 5a of one grained wheat, Triticum monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a binding site for ZCCT1 termed the CARG box. Also included are a vector comprising the recombinant ZCCT1 protein coding sequence above, a cell comprising the vector, a transgenic plant comprising the recombinant ZCCT1 protein coding sequence above (or a genetic construct that inhibits ZCCT1 repression of AP1), a seed from the transgenic plant, a method for altering a plant's response to vernalisation and a molecular marker for vrn2 derived from ADS19577. The genetic construct is an interference RNA construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding a repression defective ZCCT1 protein operably linked to a promoter or a nucleic acid sequence encoding a DNA binding defective ZCCT1 protein operably linked to a promoter. The present sequence is a plant ZCCT cDNA sequence.

Query Match 45.1%; Score 449; DB 13; Length 639;
 Best Local Similarity 84.5%; Pred. No. 8.5e-124;
 Matches 54; Conservative 0; Mismatches 85; Indels 15; Gaps 3;

109	ATGTCCATGTCATGCGGTTTGTGGCGGCCCAACAACTGCCCGCGCCTCATGTGTCGGCC	168
Qy		
1	ATGTCCATGTCATGTGTTTGTGGCGGCCAGCAACTGGCGTACCAATGATGTCGCC	60
Db		
169	ATTCCACCATCATCATCAACCATCATCAGAGAGCACAGCTGTGTGAGTACAGTTCTTCGCC	228
Qy		
61	GTTCCTCTTCATCATCAACCATCATCAGAGAACACCCACTGACAGGATACCACTTCTTCGCC	120
Db		
229	CATGGCAACCAACCAACCAACCACTATGGCTGTGGGAGCAGACTACCCAGTGCACCG---	285
Qy		
121	CAAGG-----TCACCAACCAACCAACAGCGCGGCGGAGTACCCACCAACCAACCGCA	174
Db		
286	CCGCCAGACAACCTTCGACCAACCGCAGAAACATGGACCAAGACCATTTTCATGAACACGACGG	345
Qy		


```
DT 30-DEC-2004 (first entry)
XX Langdon (tetraploid) wheat ZCCT2 genomic DNA.
XX
XX Wild emmer wheat; ds; APETALA1; API; vernalisation; flowering; ZCCT1;
KW ZCCT2; vrnl; vrn2; CARG box; plant; gene.
XX
XX Triticum turgidum; subsp. dicoccoides.
OS
XX US2004205848-A1.
XX
XX 14-OCT-2004.
XX
XX 26-NOV-2003; 2003US-00723947.
XX
XX 11-APR-2003; 2003US-00412137.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Dubcovsky J, Yan L, Loukoianov A;
XX
XX WPI; 2004-728059/71.
XX
XX P-PSDB; ADS19588.
XX
XX New recombinant ZCCT1 protein coding sequence useful for altering a
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.
XX
XX Disclosure; SEQ ID NO 84; 115pp; English.
XX
XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
CC domain protein) coding sequence comprising a nucleic acid that hybridises
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
CC the identification of to genes, vrnl identified as API (APETALA1) and
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
CC have been localised to chromosome 5a of one grained wheat, Triticum
CC monococcum. ZCCT1 is the repressor of API whose promoter contains a
CC binding site for ZCCT1 termed the CARG box. Also included are a vector
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell
CC comprising the vector, a transgenic plant comprising the recombinant
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits
CC ZCCT1 repression of API), a seed from the transgenic plant, a method for
CC altering a plant's response to vernalisation and a molecular marker for
CC Vrnl derived from ADS19577. The genetic construct is an interference RNA
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
CC a repressor defective ZCCT1 protein operably linked to a promoter or a
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
CC operably linked to a promoter. The present sequence is a plant ZCCT
CC genomic DNA sequence.
XX
XX Sequence 3454 BP; 962 A; 796 C; 716 G; 980 T; 0 U; 0 Other;
SQ
Query Match 32.2%; Score 320.8; DB 13; Length 3454;
Best Local Similarity 77.4%; Pred. No. 6.8e-85;
Matches 432; Conservative 0; Mismatches 62; Indels 64; Gaps 1;
QY 436 GTGCCATTTCGGAGTGCATCCACACATATTAGCAATGACGATCATGACTATT 495
DB 2645 GTGCCATTTCGGAGTGCATTCACGACACTATTAGCAATGACGATCATGACTATT 2704
QY 496 GACACAGAGATGATGTGGGGCTGCCCATTTATCCCAATGACGAGAGAGCGAGAG 555
DB 2705 GATACAGAGATGATGTGGGGCTGCCCATTTATCTGACGATGACGAGAGAGCGAG 2764
QY 556 GTGATGAGTATAGGAGAGAGAGAGAGCGCGCTATGACAGCAAAATCCGATACGAG 615
DB 2765 GTGATGAGTATAGGAGAGAGAGAGAGAGCGCGTGTATGACAGCAAAATCCGATACG 2824
QY 616 TCCAGAAAGCTTACCTGAGTTCGGCCATCGGTCACGCGCTTTCTCAAGGTACCC 675
DB 2825 TCCAGAAAGCTTACGCGGAGCTCAGGCCACGGGTCAATGGCGCTTTGTCAAGGTACCA 2884
```

```
676 GAAGCCATGGCATGCCCATCATCTCCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC 735
2885 GAAGCCGCTGCATCGTCTGCACCCCGCAGCTTCGCCCTATGATCCTAGTAAACTTCACCTC 2944
736 GGATGGTTCGGTAATTTATAGCACACAGCCAGATAAATGATAATATTTCTTCTGTAT 795
2945 GGATGGTTCGGTAGTTT----- 2962
796 TCATCCACCCGCGAAGCAGTGTGTTCTCAAAGTAAATAAGTCGGTTAGTATGATCGA 855
2963 -----TTCAACAAGTAATAAGTTGGTTATTTGTTGACCGA 3000
856 TTGAGGACCATTTATGTTGACTTGACTATTTAAATGGTCAGCAGATCAATCAAAACAAATG 915
3001 TGGGAGGAGTTATGTTGATTTGACTATTTCAAAGGTGACGACCAATCAAAAGAAATG 3060
916 TATTATTGAACAAGTCTGTTATACCTACGTGTTGATTAAACATGTAATTTCAAGAGG 975
3061 TATTGTTGAACAAGTATGTTATGCTTTTAAATTAAGCATGATGTTTGGAGG 3120
976 ATAGCTACTTTGATGTGT 993
3121 CTAGCTACTTAGATGTGT 3138
RESULT 10
ADS19583
ID ADS19583 standard; DNA; 5734 BP.
XX
XX AC ADS19583;
XX
XX 30-DEC-2004 (first entry)
XX
XX One grained wheat DV92 ZCCT2 genomic DNA.
XX
XX One grained wheat; chromosome 5a; ds; APETALA1; API; vernalisation;
KW flowering; ZCCT1; ZCCT2; vrnl; vrn2; CARG box; plant; gene.
XX
XX Triticum monococcum.
XX
XX US2004205848-A1.
XX
XX 14-OCT-2004.
XX
XX 26-NOV-2003; 2003US-00723947.
XX
XX 11-APR-2003; 2003US-00412137.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Dubcovsky J, Yan L, Loukoianov A;
XX
XX WPI; 2004-728059/71.
XX
XX P-PSDB; ADS19585.
XX
XX New recombinant ZCCT1 protein coding sequence useful for altering a
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.
XX
XX Disclosure; SEQ ID NO 81; 115pp; English.
XX
XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
CC domain protein) coding sequence comprising a nucleic acid that hybridises
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
CC the identification of to genes, vrnl identified as API (APETALA1) and
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
CC have been localised to chromosome 5a of one grained wheat, Triticum
CC monococcum. ZCCT1 is the repressor of API whose promoter contains a
CC binding site for ZCCT1 termed the CARG box. Also included are a vector
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell
CC comprising the vector, a transgenic plant comprising the recombinant
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits
CC ZCCT1 repression of API), a seed from the transgenic plant, a method for
CC altering a plant's response to vernalisation and a molecular marker for
CC Vrnl derived from ADS19577. The genetic construct is an interference RNA
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
CC a repressor defective ZCCT1 protein operably linked to a promoter or a
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
CC operably linked to a promoter. The present sequence is a plant ZCCT
CC genomic DNA sequence.
XX
XX Sequence 3454 BP; 962 A; 796 C; 716 G; 980 T; 0 U; 0 Other;
SQ
Query Match 32.2%; Score 320.8; DB 13; Length 3454;
Best Local Similarity 77.4%; Pred. No. 6.8e-85;
Matches 432; Conservative 0; Mismatches 62; Indels 64; Gaps 1;
QY 436 GTGCCATTTCGGAGTGCATCCACACATATTAGCAATGACGATCATGACTATT 495
DB 2645 GTGCCATTTCGGAGTGCATTCACGACACTATTAGCAATGACGATCATGACTATT 2704
QY 496 GACACAGAGATGATGTGGGGCTGCCCATTTATCCCAATGACGAGAGAGCGAGAG 555
DB 2705 GATACAGAGATGATGTGGGGCTGCCCATTTATCTGACGATGACGAGAGAGCGAG 2764
QY 556 GTGATGAGTATAGGAGAGAGAGAGAGCGCGCTATGACAGCAAAATCCGATACGAG 615
DB 2765 GTGATGAGTATAGGAGAGAGAGAGAGAGCGCGTGTATGACAGCAAAATCCGATACG 2824
QY 616 TCCAGAAAGCTTACCTGAGTTCGGCCATCGGTCACGCGCTTTCTCAAGGTACCC 675
DB 2825 TCCAGAAAGCTTACGCGGAGCTCAGGCCACGGGTCAATGGCGCTTTGTCAAGGTACCA 2884
```


Best Local Similarity	62.9%;	Pred. No. 9.1e-17;	
Matches 144;	Conservative	0;	Mismatches 85; Indels 0; Gaps 0;
QY	531	CACAATGCGAGGAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGGAGCGCGC	590
Db	770	CGCAATGGTGGAGGGAGGCCAAGCTGATGAGGTACAGGAGAGAGGAGAGAGGTG	829
QY	591	CTATGACAAGCAAAATCCGATACGAGTCCAGAAAGCTTTACGCTGAGCTTCGGCCATGGT	650
Db	830	CTACGAGAGCAAAATCCGGTACCGTCCAGAAAGCCCTATGCCAGATGAGGCCCGAGT	889
QY	651	CAAGGCCGCTTTGTGTCNAGGTACCGAGCCATGGCATCGCCATCATCTCCAGCTTCGCC	710
Db	890	GAGAGTTCGCTTCGCCAAAGAACTGATCAGGAAGCTGTCCACCGCCATCCACCTATGT	949
QY	711	CTATGATCCTTAGTAAACTTCACCTCGGATGGTTCGGGTAATTTATAGCA	759
Db	950	CGATCTAGTAGCTTCGAGCTTGACCAATGGTTCAGATAGATAATTACA	998
RESULT 15	Lhd4-related Oryza sativa cDNA sequence SeqIDS.		
ADSI6783	ID ADS16783 standard; cDNA; 1078 BP.		
XX	AC	ADS16783;	
XX	XX	16-DEC-2004 (first entry)	
DE	Lhd4-related Oryza sativa cDNA sequence SeqIDS.		
XX	Lhd4;	plant flowering; flowering time; efficient development;	
KW	rice growth; gene; ss.		
XX	Oryza sativa.		
XX	WO2004081210-A1.		
XX	23-SEP-2004.		
XX	10-MAR-2004;	2004WO-JP003122.	
XX	PF		
XX	XX	10-MAR-2003;	2003JP-00063960.
XX	(PLAN-) PLANT GENOME CENT CO LTD.		
PA	(PLAN-) PLANT FUNCTIONAL GENOMICS CO LTD.		
XX	Minobe Y, Monna L, Kitazawa N, Maehara Y, Masuda H, Yano M;		
PI	WPI; 2004-677545/66.		
DR	P-PSDB; ADS16784.		
XX	New gene Lhd4 encoding a protein capable of delaying flowering in a		
PT	plant, useful for controlling flowering time in rice.		
XX	Example 1; SEQ ID NO 5; 124pp; Japanese.		
PS	This invention relates to a novel DNA, designated Lhd4 and encoding a		
XX	protein capable of delaying flowering in a plant. The invention is useful		
CC	for delaying flowering of a plant, which comprises expressing the novel		
CC	DNA within the cells of a plant, such as rice. The Lhd4 protein enables		
CC	control of flowering time of a plant, such as rice, thus causing		
CC	efficient development and growth of an excellent variety. The present		
CC	sequence is that of an Oryza sativa cDNA which was used in the		
CC	exemplification of the invention.		
XX	Sequence 1078 BP; 224 A; 309 C; 317 G; 228 T; 0 U; 0 Other;		
SQ	Query Match	9.3%;	Score 93; DB 13; Length 1078;
	Best Local Similarity	62.9%;	Pred. No. 9.1e-17;
	Matches 144;	Conservative	0; Mismatches 85; Indels 0; Gaps 0;
QY	531	CACAATGCGAGGAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGGAGCGCGC	590


```

Db      770  CGCAATGGTGGAGAGGGAGGCCAAGCTGATGAGGTACAAGGAGAGAGGAGAGAGGAGGTS 829
Qy      591  CTATGACAAAGCAAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGT 650
Db      830  CTACGAGAGCAANTCCGGTACGCTCCAGAAAAGCTTATGCCGAGATGAGGCCCGGAGT 889
Qy      651  CAACGGCCGCTTTGTCAAGGTACCCGAAGCCATGGCATCGCCCATCATCTCCAGCTTCGCC 710
Db      890  GAGAGTCCGCTTCGCCCAAGAACCTGATCAGGAAGCTGTGCGACCGCCATCCACCTATGT 949
Qy      711  CTATGATCCTAGTAAACTTCACCTCGATGGTTCGGTAAATTATAGCA 759
Db      950  CGATCCTAGTAGGCTTGAGCTTGGACAATGGTTTCAGATAGATAATTACA 998

```

Search completed: February 23, 2006, 12:16:19
Job time : 719 secs


```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; CLONE: ptzgt-F1s
; IMMEDIATE SOURCE:
US-08-232-463-14

Query Match
Best Local Similarity 4.8%; Score 47.4; DB 2; Length 7218;
Matches 15; Conservative 207; Mismatches 153; Indels 0; Gaps 0;

QY 310 AGAACATGACAGACCATTTCATGAACAGCAGCGGCAGGCAACAGCAGCAGCGCTCACG 369
DB 1412 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1353
QY 370 CTGGAGGTGGCGCAGCGCCAAACACATGCTCACCTAGTGCAGCCACCGCAGAGGCC 429
DB 1352 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1293
QY 430 CACATCGTGCCATTTCACGAGGTGCATTCACAACATATAGCAATGAGCAATCATG 489
DB 1292 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1233
QY 490 ACTATTGACACAGATGATGTGGGCTGCCATTATCCACATCCAGAGAGCA 549
DB 1232 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1173
QY 550 GCGAAGGTGATAGGATAGGAGAAGAGAGAGCGCGCTATGACAAACATCGA 609
DB 1172 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1113
QY 610 TAGAGTCCAGAAAAGCTTACGCTAGCTGCGCATGGTCAACGCGCTTTGTCAAG 669
DB 1112 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1053
QY 670 GTACCCGAGCCATG 684
DB 1052 CGACTCGACGCAAG 1038

RESULT 7
US-09-949-016-13845/c
; Sequence 13845, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12371
; LENGTH: 152145
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13845

Query Match
Best Local Similarity 4.6%; Score 45.6; DB 3; Length 152145;
Matches 93; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 138 CAACAACCTGCCCGCCTCATGTCTCGCCCATTCACCATCATCATCATCATCATGGA 197
DB 136799 CCACCACCACCAACCACTCCACCAACCAACCAACCAACCAACCAACCAACCA 136740
QY 198 GCACCAAGCTGTGTGAGTACCAAGTTCTTCCCATGGCAACCAACCAACCAACCA 257
DB 136739 CCACCACCTCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 136680
QY 258 CTCGGCAGCAGACTACCCAGTCCACCGCGCCAGACAACTTCGACCAACCGC 309
DB 136679 CCACCACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 136628

RESULT 8
US-09-949-016-12371/c
; Sequence 12371, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12371
; LENGTH: 152145
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12371

Query Match
Best Local Similarity 4.6%; Score 45.6; DB 3; Length 152145;
Matches 93; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

QY 138 CAACAACCTGCCCGCCTCATGTCTCGCCCATTCACCATCATCATCATCATGGA 197
DB 136799 CCACCACCACCAACCACTCCACCAACCAACCAACCAACCAACCAACCAACCA 136740
QY 198 GCACCAAGCTGTGTGAGTACCAAGTTCTTCCCATGGCAACCAACCAACCAACCA 257
DB 136739 CCACCACCTCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 136680
QY 258 CTCGGCAGCAGACTACCCAGTCCACCGCGCCAGACAACTTCGACCAACCGC 309
DB 136679 CCACCACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 136628

RESULT 9
US-09-949-016-103758/c
; Sequence 103758, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

```

Query Match	4.5%	Score 45.2;	DB 3;	Length 30656;
Best Local Similarity	54.1%;	Pred.No. 0.031;		
Matches	92; Conservative	0; Mismatches	78; Indels	0; Gaps . 0;
QY	138	CACAACTGCCGGCCTCATGTTCTCGCCATTTCACCATCATCACCATCATCATGGA	197.	
DB	3723	CGATCACTACCACATCACAAATCAGCAGCACGACACAACACCATCACCAACCACTA	3664	

```

RESULT 12
US-10-148-806-3
; Sequence 3, Application US/10148806
; Patent No. 6762042
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; TITLE OF INVENTION: HELICASE
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 114793
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-148-806-3

```


Search completed: February 23, 2006, 12:04:39
Job time : 198 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 23, 2006, 12:00:04 ; Search time 4762 Seconds
(without alignments)
9785.790 Million cell updates/sec

Title: US-10-723-947-75

Perfect score: 996

Sequence: 1 taactgcctctctctctcc.....tagctacttgatggtgaat 996

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_hic:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_est7:*
- 9: gb_gss1:*
- 10: gb_gss2:*
- 11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
C 1	95.8	9.6	364	9	CC647520	CGPA002TH
C 2	95.8	9.6	833	9	BZ734187	OGFAQ22TC
C 3	95.8	9.6	1021	10	CL012630	ZMMBBB053
C 4	94.8	9.5	761	9	CC728227	OGCCY57TM
C 5	94.8	9.5	850	9	CC685007	OGAS10TV
C 6	94.8	9.5	907	9	CC685002	OGAS10TH
C 7	94.8	9.5	1006	10	CL983403	ZMMBHa000
C 8	92.6	9.3	848	7	CV291360	aof01-5ms
C 9	91.2	9.2	864	10	CL972569	OsIFCC023
C 10	90.4	9.1	640	10	CL925503	OA_ABA003
C 11	90.4	9.1	726	9	CC879645	ZMMBBb021
C 12	89	8.9	736	10	CL149066	104_329_1
C 13	88.8	8.9	741	9	BZ679381	PUBSI88TD
C 14	77.2	7.8	689	8	DN238319	MUC4LH100
C 15	77.2	7.8	1061	7	CK163737	FGAS01636
C 16	76.6	7.7	410	1	AV805290	AV805290
C 17	76.6	7.7	460	1	AV785412	AV785412
C 18	76.6	7.7	484	1	AV519830	AV519830
C 19	76.6	7.7	560	6	CD530587	06P03_Ara
C 20	76.6	7.7	631	1	AV538590	AV538590
C 21	76.6	7.7	832	8	DR749947	84-I02059
C 22	76.6	7.7	1088	4	CNS09YA6	BX841997 Arabidops

23	76.6	7.7	1113	4	CNS0A8F5	BX819991 Arabidops
24	76.6	7.7	1120	4	CNS0Y9F	BX842081 Arabidops
25	76.4	7.7	510	2	BE039045	BE039045 Arabidops
C 26	76.4	7.7	580	8	CX114723	CX114723 Arabidops
C 27	76.2	7.7	319	6	CB684050	CB684050 Arabidops
C 28	76.2	7.7	465	10	CL953070	CL953070 Arabidops
29	75.8	7.6	547	7	CF954823	CF954823 Arabidops
30	75.8	7.6	571	7	CF954930	CF954930 Arabidops
31	75.8	7.6	648	7	CK084516	CK084516 Arabidops
C 32	75.6	7.6	516	3	BJ455277	BJ455277 Arabidops
33	75.6	7.6	536	6	CA592838	CA592838 Arabidops
34	75.6	7.6	536	6	CA592641	CA592641 Arabidops
35	75.6	7.6	538	3	BJ447520	BJ447520 Arabidops
36	75.6	7.6	568	8	DN178125	DN178125 Arabidops
C 37	75.6	7.6	841	2	BF264488	BF264488 Arabidops
C 38	75.4	7.6	400	8	DN185034	DN185034 Arabidops
C 39	75.4	7.6	500	6	CB663843	CB663843 Arabidops
C 40	75.4	7.6	502	7	CK036170	CK036170 Arabidops
41	75.4	7.6	516	1	AU056338	AU056338 Arabidops
C 42	75.4	7.6	582	6	CB686036	CB686036 Arabidops
C 43	75.4	7.6	606	7	CF952821	CF952821 Arabidops
C 44	75.4	7.6	653	6	CB684028	CB684028 Arabidops
C 45	75.4	7.6	674	6	CB677083	CB677083 Arabidops

ALIGNMENTS

RESULT 1
CC647520/c
LOCUS CC647520 364 bp DNA linear GSS 19-JUN-2003
DEFINITION CGPA002TH ZM.0.7.1.5 KB Zea mays genomic clone ZMMBMA0351B03,
genomic survey sequence.
ACCESSION CC647520
VERSION CC647520.1 GI:32048648
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T., Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
TITLE Consortium for Maize Genomics
JOURNAL Unpublished (2002)
COMMENT Other_GSSs: CGPA002TV
Contact: Cathy Whitelaw

FEATURES

source
1..364
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0351B03"
/clone_lib="ZM.0.7.1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 9.6%; Score 95.8; DB 9; Length 364;
Best Local Similarity 65.6%; Pred.No. 5e-15;
Matches 158; Conservative 0; Mismatches 77; Indels 6; Gaps 1;
Oy 540 GGAGAGACGACGAGAGGTGATGAGGTATAGGAGAGAGAGAGCGCGCTATGACAA 599

```

Db      305  GGACCGGAGCGGAAGGTGATCGGTACAGGAGAAAGCGGAAGAGGCGCTACAGAA 246
QY      600  GCAATCCGATACAGATCCAGAGAAAGCTTACGCTGAGCTTCGGCCATGGTCAACGGCGG 659
Db      245  GCAGATTCGTAGCCCTCCCGCAAGGCTATGAGAGATCGGCGCGGTCAAGGGCGG 186
QY      660  CTTTGTCAAGGTACCGCAAGCCATGGCATCG-----CCATCATCTCCAGCTTCGCCCTA 713
Db      185  CTTTCGCAAGGTCCCGACGCTGAGGCTCGCTCGCCACCGCGCGCGCGCATGCTA 126
QY      714  TGATCTAGTAACCTTACCTCGATGGTTCGGTATTTATAGCAACAGCCAGATATAA 773
Db      125  CGAACAGGCGCGCTCGACCTCGATGGTTCGGTTCATAGCAAAAGAGGCCACTGGTTAA 66
QY      774  T 774
Db      65  T 65

RESULT 2
LOCUS      BZ734187/c
DEFINITION BZ734187 833 bp DNA linear GSS 03-MAR-2003
            OGA222TC ZM 0.7_1.5_KB Zea mays genomic clone ZMBMa0241C19,
            genomic survey sequence.
ACCESSION  BZ734187
VERSION    BZ734187.1 GI:28710795
KEYWORDS   GSS.
SOURCE     Zea mays
            Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 833)
AUTHORS    Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
            Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
            Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
            Consortium for Maize Genomics
            Unpublished (2002)
            Other GSSs: OGA222TM
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: methylation filtered.
            Location/Qualifiers
FEATURES   source
            1..833
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone="ZMBMa0241C19"
                /clone_lib="ZM 0.7_1.5_KB"
                /note="Vector: pBCK-; Site_1: HincII; 0.7-1.5 kb
                methylation filtered genomic DNA library"

ORIGIN
Query Match      9.6%; Score 95.8; DB 9; Length 833;
Best Local Similarity 65.6%; Pred. No. 6.1e-15;
Matches 158; Conservative 0; Mismatches 77; Indels 6; Gaps 1;

QY      540  GGAGAGCAGCGCAAGGTGATGAGGTATAGGAGAGAGCAAGCGCGGCTATCAGAA 599
Db      552  GGACGGGAGCGCAAGGTGATGCGGTACAGGAGAGCGCAAGAGAGGCGGCTACAGAA 493
QY      600  GCAATCCGATACAGATCCAGAGAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCGG 659
Db      492  GCAGATTCGTAGCCCTCCCGCAAGGCTATGAGAGATGCGCGCGGTCAAGGGCGG 433
QY      660  CTTTGTCAAGGTACCGCAAGCCATGGCATCG-----CCATCATCTCCAGCTTCGCCCTA 713


```

```

Db      432  CTTCCGCAAGTGGCCGCGGTCGAGGCTCCGTCGCCACCGCGCGCGCATGCTA 373
QY      714  TGATCTAGTAACCTTACCTCGATGGTTCGGTAAATTTATAGCAACAGCCAGATATAA 773
Db      372  CGAACCGAGCGCGCTCGACCTCGGATGGTTCGTTTCATAGCAAGAGGCCACTGGTTAA 313
QY      774  T 774
Db      312  T 312

RESULT 3
LOCUS      CL012630/c
DEFINITION ZMBBBb0537C10r ZMBBBb 1021 bp DNA linear GSS 29-DEC-2003
            ZMBBBb0537C10 3', genomic survey sequence.
ACCESSION  CL012630
VERSION    CL012630
KEYWORDS   GSS.
SOURCE     Zea mays
            Zea mays
ORGANISM   Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 1021)
AUTHORS    Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
            Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.
            Sequencing of the maize genome at PGIR (2003c)
            Unpublished (2003)
            Contact: Bharti, A.K.
            Dr. Joachim Messing's lab
            The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
            University
            190 Frelinghuysen Road, Piscataway, NJ 08854, USA
            Tel: 732 445 3801
            Fax: 732 445 5735
            Email: bharti@waksman.rutgers.edu
            Seq primer: SP6
            Class: BAC ends
            High quality sequence start: 9.
            Location/Qualifiers
FEATURES   source
            1..1021
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /cultivar="B73"
                /db_xref="taxon:4577"
                /clone="ZMBBBb0537C10"
                /lab_host="E. coli DH10B"
                /clone_lib="ZMBBBb (HindIII)"
                /note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      9.6%; Score 95.8; DB 10; Length 1021;
Best Local Similarity 65.6%; Pred. No. 6.5e-15;
Matches 158; Conservative 0; Mismatches 77; Indels 6; Gaps 1;

QY      540  GGAGAGCAGCGCAAGGTGATGAGGTATAGGAGAGAGCAAGAGCGCGGCTATGACAA 599
Db      276  GGACCGGAGCGCAAGGTGATGCGGTACAGGAGAGCGCAAGAGAGGAGCGGCTACGAGAA 217
QY      600  GCAATCCGATACAGATCCAGAGAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCGG 659
Db      216  GCAGATTCGTAGCCCTCCCGCAAGGCTATGAGAGATGCGCGCGGTCAAGGGCGG 157
QY      660  CTTTGTCAAGGTACCGCAAGCCATGCGATCG-----CCATCATCTCCAGCTTCGCCCTA 713
Db      156  CTTCCGCAAGGTGCGCGGACGCTGAGGCTCCGTCCGCCACCGCGCGCGCATGCTA 97
QY      714  TGATCTAGTAACCTTACCTCGGATGGTTCGGTAAATTTATAGCAACAGCCAGATATAA 773
Db      96  CGAACCGAGCGCGCTCGACCTCGGATGGTTCGTTTCATAGCAAGAGGCCACTGGTTAA 37


```

```

QY 774 T 774
Db 36 T 36

RESULT 4
CC728227/c
LOCUS CC728227 761 bp DNA linear GSS 23-JUN-2003
DEFINITION OGCCV57TM ZM_0.7_1.5_KB Zea mays genomic clone ZM5BMA0146117,
genomic survey sequence.
ACCESSION CC728227
VERSION CC728227.1 GI:32147160
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 761)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
TITLE JOURNAL
COMMENT Other GSSs: OGCCV57TC
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1..761
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM5BMA0146117"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES
source
1..761
Query Match 9.5%; Score 94.8; DB 9; Length 761;
Best Local Similarity 67.0%; Pred. No. 1.1e-14;
Matches 154; Conservative 0; Mismatches 67; Indels 9; Gaps 1;

QY 540 GGAGAGCAGCGAAGTGATGAGGTATAGGAGAGAGAGAGAGCGCGCTATGACAA 599
Db 540 GGACCGGGAGGCGAAGGTATCGGTACAGAGAGAGAGAGAGCGCGCTACGAGAA 481

QY 600 GCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGCCATCCAGCGCGC 659
Db 480 GCAGATTGCTACGCTTCCCGTAGCGGTACGGGAGATCGCGCGCGCTCAAGGGCGC 421

QY 660 CTTTGTCAAGGTACCGGAAG-----CCATGCGATCGCCATCATCTCCAGCTTCGCC 710
Db 420 CTTCCGAAGGTGCCGACGGTGATGCTCCCGCGCCACCGCGCGCGCTGCGGGGG 361

QY 711 CTATGATCCTAGTAACCTCACCTCGGATGTTCCGGTAATTATAGCAC 760
Db 360 CTACGAACCAAGCGCGCTCGACCTCGGATGTTCCGTTTCATAGCAACAC 311

RESULT 5
CC685007
LOCUS CC685007 850 bp DNA linear GSS 19-JUN-2003
DEFINITION OGAS10TV ZM_0.7_1.5_KB Zea mays genomic clone ZM5BMA0340B19,
genomic survey sequence.
ACCESSION CC685007
VERSION CC685007.1 GI:32089783
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 850)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
TITLE JOURNAL
COMMENT Other GSSs: OGAS10TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
Location/Qualifiers
1..850
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM5BMA0340B19"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES
source
1..850
Query Match 9.5%; Score 94.8; DB 9; Length 850;
Best Local Similarity 67.0%; Pred. No. 1.2e-14;
Matches 154; Conservative 0; Mismatches 67; Indels 9; Gaps 1;

QY 540 GGAGAGCAGCGAAGTGATGAGGTATAGGAGAGAGAGAGCGCGCTATGACAA 599
Db 509 GGACCGGGAGGCGAAGGTATCGGTACAGAGAGAGAGAGAGCGCGCTACGAGAA 568

QY 600 GCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGCCATCCAGCGCGC 659
Db 569 GCAGATTGCTACGCTTCCCGTAGCGGTACGGGAGATCGCGCGCGCTCAAGGGCGC 628

QY 660 CTTTGTCAAGGTACCGGAAG-----CCATGCGATCGCCATCATCTCCAGCTTCGCC 710
Db 629 CTTCCGAAGGTGCCGACGGTGATGCTCCCGCGCCACCGCGCGCGCTGCGGGGG 688

QY 711 CTATGATCCTAGTAACCTCACCTCGGATGTTCCGGTAATTATAGCAC 760
Db 689 CTACGAACCAAGCGCGCTCGACCTCGGATGTTCCGTTTCATAGCAACAC 738

RESULT 6
CC685002/c
LOCUS CC685002 907 bp DNA linear GSS 19-JUN-2003
DEFINITION OGAS10TH ZM_0.7_1.5_KB Zea mays genomic clone ZM5BMA0340B19,
genomic survey sequence.
ACCESSION CC685002
VERSION CC685002.1 GI:32089778
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 907)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
TITLE JOURNAL
COMMENT Other GSSs: OGAS10TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: methylation filtered.
Location/Qualifiers
1..850
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZM5BMA0340B19"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

FEATURES
source
1..850
Query Match 9.5%; Score 94.8; DB 9; Length 850;
Best Local Similarity 67.0%; Pred. No. 1.2e-14;
Matches 154; Conservative 0; Mismatches 67; Indels 9; Gaps 1;

QY 540 GGAGAGCAGCGAAGTGATGAGGTATAGGAGAGAGAGAGCGCGCTATGACAA 599
Db 509 GGACCGGGAGGCGAAGGTATCGGTACAGAGAGAGAGAGAGCGCGCTACGAGAA 568

QY 600 GCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGCCATCCAGCGCGC 659
Db 569 GCAGATTGCTACGCTTCCCGTAGCGGTACGGGAGATCGCGCGCGCTCAAGGGCGC 628

QY 660 CTTTGTCAAGGTACCGGAAG-----CCATGCGATCGCCATCATCTCCAGCTTCGCC 710
Db 629 CTTCCGAAGGTGCCGACGGTGATGCTCCCGCGCCACCGCGCGCGCTGCGGGGG 688

QY 711 CTATGATCCTAGTAACCTCACCTCGGATGTTCCGGTAATTATAGCAC 760
Db 689 CTACGAACCAAGCGCGCTCGACCTCGGATGTTCCGTTTCATAGCAACAC 738

```

COMMENT

Other_GSSs: OGAS10TV
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5943
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: methylation filtered.
Location/Qualifiers
1. .907

FEATURES

source
1. .907
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone_lib="ZMBMa0340B19"
/clone_lib="ZM 0.7 1.5 KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 9.5%; Score 94.8; DB 9; Length 907;
Best Local Similarity 67.0%; Pred. No. 1.2e-14;
Matches 154; Conservative 0; Mismatches 67; Indels 9; Gaps 1;

QY 540 GGAGAGAGCGAAGGTGATGATGATAGGGAGAGAGAGAGAGCGCGCTATGACAA 599
DB 651 GGACCGGAGGCGAGGTGATGCGGTACAGAGAGAGAGAGAGAGCGCGCTACGAGAA 592
QY 600 GCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGCCATGGTCAACGCCG 659
DB 591 GCAGATTCCGCTACGCTTCCCGTAAGCGGTACGCGGAGATCGCGCGCGCTCAAGGGCG 532
QY 660 CTTTGTCAAGGTACCCGAAG-----CCATGGCATGCCATCATCTCCAGCTTCGCC 710
DB 531 CTTCCGACAGTCCCGACGGTGATCTCCCGCGCCACAGCGCGCGCTCGGGGG 472
QY 711 CTATGATCTCTAGTAATCTTACCTCGGATGGTTCCGGTAATTATAGCAC 760
DB 471 CTACGAACCGCGCGCTCGACCTCGGATGGTTCCGTTTCATAGCAAAACAC 422

RESULT 7

CL983403
LOCUS
DEFINITION
ZMBMa0001121.f ZMBMa Zea mays genomic clone ZMBMa0001121 5',
genomic survey sequence.

ACCESSION
CL983403
VERSION
CL983403.1 GI:52551481
KEYWORDS
GSS.

SOURCE

ORGANISM
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
Clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1006)
Ma, J., SanMiguel, P., Liu, R., Haller, K., Soderlund, C. and
Bennetzen, J.

TITLE

ZMBH sequences

JOURNAL

COMMENT
Unpublished (2004)
Contact: Jeff Bennetzen
Bennetzen Lab
The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, GA
30602, USA
Tel: 706-542-3698
Fax: 706-583-0972
Email: maize@uga.edu
Plate: 0001 row: 1 column: 21
Class: BAC ends.
Location/Qualifiers
1. .1006
/organism="Zea mays"

FEATURES

source

/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMBMa0001121"
/tissue_type="immature ear"
/dev_stage="6-8 weeks"
/lab_host="DH10B"
/clone_lib="ZMBMa"
/note="Vector: TOPOpcr4; Site_1: EcoRI; Site_2: EcoRI"

ORIGIN

Query Match 9.5%; Score 94.8; DB 10; Length 1006;
Best Local Similarity 67.0%; Pred. No. 1.2e-14;
Matches 154; Conservative 0; Mismatches 67; Indels 9; Gaps 1;

QY 540 GGAGAGAGCGAAGGTGATGATGATAGGGAGAGAGAGAGAGCGCGCTATGACAA 599
DB 47 GCACCGGAGGCGAGGTGATGCGGTACAGAGAGAGAGAGAGAGCGCGCTACGAGAA 106
QY 600 GCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGCCATGGTCAACGCCG 659
DB 107 GCAGATTCCGCTACGCTTCCCGTAAGCGGTACGCGGAGATCGCGCGCGCTCAAGGGCG 166
QY 660 CTTTGTCAAGGTACCCGAAG-----CCATGGCATGCCATCATCTCCAGCTTCGCC 710
DB 167 CTTCCGACAGTCCCGACGGTGATCTCCCGCGCCACAGCGCGCGCTCGGGGG 226
QY 711 CTATGATCTCTAGTAATCTTACCTCGGATGGTTCCGGTAATTATAGCAC 760
DB 227 CTACGAACCGCGCGCTCGACCTCGGATGGTTCCGTTTCATAGCAAAACAC 276

RESULT 8

CV291360

LOCUS

DEFINITION

aof01-5msl-b04 5', mRNA sequence.

ACCESSION

CV291360

VERSION

CV291360.1 GI:52577578

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2004)

Contact: Claude dePamphilis or James Leebens-Mack

Mueller Laboratory

Penn State University

208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn

State University, University Park, PA 16802, USA

Tel: 814 863 6413

Fax: 814 865 9131

Email: cwd3@psu.edu or jhl10@psu.edu

The sequence provided is trimmed of vector and low quality regions.

Full sequence and original trace file are available from the Plant

Genome Network website (<http://pgn.cornell.edu>)

Plate: aof01-5msl row: b column: 04

Seq primer: M13F.

Location/Qualifiers

1. .848

/organism="Asparagus officinalis"

/mol_type="mRNA"

/db_xref="PCN:aof01-5msl-b04"

/db_xref="taxon:4686"

/clone="aof01-5msl-b04"

/tissue_type="male inflorescences"

Location/Qualifiers

1. .848

/organism="Asparagus officinalis"

/mol_type="mRNA"

/db_xref="PCN:aof01-5msl-b04"

/db_xref="taxon:4686"

/clone="aof01-5msl-b04"

/tissue_type="male inflorescences"

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	996	100.0	996	8	US-10-723-947-75	Sequence 75, Appl
2	907.2	91.1	975	8	US-10-723-947-79	Sequence 79, Appl
3	561	56.3	7051	8	US-10-723-947-74	Sequence 74, Appl
4	553	55.5	2913	8	US-10-723-947-78	Sequence 78, Appl
5	455.2	45.7	643	8	US-10-723-947-91	Sequence 91, Appl
6	451.4	45.3	639	8	US-10-723-947-85	Sequence 85, Appl
7	449	45.1	639	8	US-10-723-947-88	Sequence 88, Appl
8	445	44.7	639	8	US-10-723-947-82	Sequence 82, Appl
9	320.8	32.2	3454	8	US-10-723-947-84	Sequence 84, Appl
10	320.8	32.2	5734	8	US-10-723-947-81	Sequence 81, Appl
11	251.4	25.2	2043	8	US-10-723-947-90	Sequence 90, Appl
12	247.6	24.9	1985	8	US-10-723-947-87	Sequence 87, Appl
13	92.8	9.3	864	7	US-10-437-963-83163	Sequence 83163, A
14	86	8.6	1413	7	US-10-437-963-82314	Sequence 82314, A
15	76.6	7.7	885	3	US-09-938-842A-265	Sequence 265, App
16	76.6	7.7	885	3	US-09-938-842A-265	Sequence 265, App
17	76.6	7.7	1075	7	US-10-425-114-32406	Sequence 22406, A
18	76.6	7.7	1120	7	US-10-412-699B-597	Sequence 597, App
19	76.6	7.7	1141	5	US-10-295-403-107	Sequence 107, App
20	75.4	7.6	577	7	US-10-260-238-390	Sequence 390, App
21	75.4	7.6	1768	7	US-10-437-963-40	Sequence 40, Appl
22	74.8	7.5	1002	7	US-10-260-238-403	Sequence 403, App
23	74.8	7.5	2717	7	US-10-437-963-30197	Sequence 30197, A

FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-723-947-91

Query Match 45.7%; Score 455.2; DB 8; Length 642;
Best Local Similarity 83.0%; Pred. No. 2.9e-122;
Matches 533; Conservative 0; Mismatches 103; Indels 6; Gaps 1;
QY 109 ATGTCATCTCATGCGGTTTGTGCGCGCCCAACCACTGCCCGGCTCATGCTCTCGGCC 168
DB 1 ATGTCATGCGATGCGGTTTGTGCGCGCCCAACCACTGCCCGGCTCATGCTCTCGGCC 60
QY 169 ATTACCATCATCACCATCATCAGGAGCACCAGCTGTGTAGTACCACTTCTTGGCC 228
DB 61 GTTCTTCTCATCATCACCATCATCAGGAGCACCAGCTGTGTAGTACCACTTCTTGGCC 120
QY 229 CATGGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 288
DB 121 CAAGGTCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 180
QY 289 CCAGCACTTTCAGACCGCAGACCATGAGCCAGACCACTTTCATGAACAGCAGCGGCA 348
DB 181 CCGGCCAATTGCGCCAGATCATGGGCGCAGCTGTTCATGAACAGCAGCTCCA 240
QY 349 GGGAAACAGCAGCGGCTCAAGTGTGGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCG 408
DB 241 GTGATAGCAGCAGGCTCACACAGAGGTGGAGCGGCGGCGGCGGCGGCGGCGGCGGCG 300
QY 409 GTGAGCCACCGG-----CAAGAGCCACATGTCGCCATTTTCAAGAGTGCATTCACC 462
DB 301 CTGCAAGCCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 463 AACCTATTAGCAATGACGATCATGACTATTGACAGAGATGATGATGATGATGATGATGAT 522
DB 361 AACCTATTAGCAATGACGATCATGACTATTGACAGAGATGATGATGATGATGATGATGAT 420
QY 523 CATTATCCCAATGACAGAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGAGAGAGAG 582
DB 421 TATAGTCCAAAGTACAG 480
QY 583 AGCGGCGCTATGACAAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGG 642
DB 481 AAGCGGCGCTATGACAAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGG 540
QY 643 CCATGGGTCAAGCGCGCTTTGTCAAGGTACCGAAGCCATGGCATCGCATCATCTCCA 702
DB 541 CCACGGGTCAAGCGCGCTTTGTCAAGGTACCGAAGCCATGGCATCGCATCATCTCCA 600
QY 703 GCTTCGCCCTATGATCTAGTAACTTACCTCGGATGGTTC 744
DB 601 GCTTCGCCCTATGATCTAGTAACTTACCTCGGATGGTTC 642

RESULT 6
US-10-723-947-85
; Sequence 85, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; FILE REFERENCE: 514112000320

; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Triticum dicoccoides
US-10-723-947-85

Query Match 45.3%; Score 451.4; DB 8; Length 639;
Best Local Similarity 83.6%; Pred. No. 3.7e-121;
Matches 541; Conservative 0; Mismatches 91; Indels 15; Gaps 2;
QY 109 ATGTCATCTCATGCGGTTTGTGCGCGCCCAACCACTGCCCGGCTCATGCTCTCGGCC 168
DB 1 ATGTCATCTCATGCGGTTTGTGCGCGCCCAACCACTGCCCGGCTCATGCTCTCGGCC 60
QY 169 ATTACCATCATCACCATCATCAGGAGCACCAGCTGTGTAGTACCACTTCTTGGCC 228
DB 61 GTTCT-----TCAGCATCAGGAACAACACCGGCTGCGGAGTACCACTTCTTACC 111
QY 229 CATGGAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 288
DB 112 CAAGGTCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 171
QY 289 CCAGCACTTTCAGACCGCAGACCATGAGCCAGACCACTTTCATGAACAGCAGCGGCA 348
DB 172 TCAGCAATTCGCAACCATGCGATCATGAGACCAACCGTTTTCATGAACAGCAGCTCCA 231
QY 349 GGGAAACAGCAGCGGCTCAAGTGTGGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCG 408
DB 232 GGGAAACAGCAGCGGCTCAAGTGTGGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCG 291
QY 409 GTGAGCCACCGG-----CAAGAGCCACATGTCGCCATTTTCAAGAGTGCATTCACC 462
DB 292 CTGCAAGCCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 351
QY 463 AACCTATTAGCAATGACGATCATGACTATTGACAGAGATGATGATGATGATGATGATGAT 522
DB 352 AGCACTATTAGCAATGACGATCATGACTATTGACAGAGATGATGATGATGATGATGATGAT 411
QY 523 CATTATCCCAATGACAGAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGAGAGAGAG 582
DB 412 CATAATCTGACGATGACAG 471
QY 583 AGCGGCGCTATGACAAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGG 642
DB 472 AGCGGCGCTATGACAAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCAGG 531
QY 643 CCATGGGTCAAGCGCGCTTTGTCAAGGTACCGAAGCCATGGCATCGCATCATCTCCA 702
DB 532 CCACGGGTCAAGCGCGCTTTGTCAAGGTACCGAAGCCATGGCATCGCATCATCTCCA 591
QY 703 GCTTCGCCCTATGATCTAGTAACTTACCTCGGATGGTTC 749
DB 592 GCTTCGCCCTATGATCTAGTAACTTACCTCGGATGGTTC 638

RESULT 7
US-10-723-947-88
; Sequence 88, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947

RESULT 9
US-10-723-947-84
; Sequence 84, Application US/10723947
; Publication No. US20040205848A1.
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137

```
; -PRIOR FILING DATE: 2003-04-11
; -NUMBER OF SEQ ID NOS: 159
; -SOFTWARE: FastSeq for Windows Version 4.0
; -SEQ ID NO 84
; -LENGTH: 3454
; -TYPE: DNA
; -ORGANISM: Triticum dicoccoides
; -US-10-723-947-84

Query Match      32.2%; Score 320.8; DB 8; Length 3454;
Best Local Similarity 77.4%; Pred. No. 1.7e-82;
Matches 432; Conservative 0; Mismatches 62; Indels 64; Gaps 1;

QY 436 GTGCCATTTCCAGGAGTGCATTCAACAACACTATTAGCAATGAAGCAATCATGACTATT 495
Db 4005 GTGCCATTTCCGGGGCTGCATTCCACGACTATTAGCAATGAACATCATGACTATT 4064
QY 496 GACACAGAGATGATGTGGGGCTGCCCATTTATCCACAATTCAGAGAGAGAGCGAAG 555
Db 4065 GATACAGAGATGATGTGGGGCTGCCCATTAATTCGACGATTCAGAGAGAGAGCGAAG 4124
QY 556 GTGATGAGGTATAGGAGAGAGAGAGAGAGCGCGCTATGACAAAGCAAAATCCGATACGAG 615
Db 4125 GTGATGAGGTATAGGAGAGAGAGAGAGAGCGCGTCTATGACAAAGCAAAATCCGCTACGAG 4184
QY 616 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATCGGTCACGCGCGCTTTGTCAAGGTACCC 675
Db 4185 TCCAGAAAAGCTTACGCGAGCTTCAGGCAACGCTGCTTTGTCAAGGTACCA 4244
QY 676 GAAGCCATGCGCATCATCTCCAGCTTCGCGCTATGATCCTTAGTAACTTCACCTC 735
Db 4245 GAAGCGCTGCTCGTCCGCTCAGCTTCGCGCTATGATCCTTAGTAACTTCACCTC 4304
QY 736 GGATGTTCCGGTAATTTATAGCACAGCCAGATAAAATGATAATTCCTCTGAT 795
Db 4305 GGATGTTCCGTAATTTATAGCACAGCCAGATAAAATGATAATTCCTCTGAT 4322
QY 796 TGATCCACCGTGAAGAGCAGTTGTTCTCTCAAAAGTAAATAGTCGGTTAGTATCGA 855
Db 4323 TGATCCACCGTGAAGAGCAGTTGTTCTCTCAAAAGTAAATAGTGGTTATGTTGACCGA 4360
QY 856 TTGGAGCCATTATGTTGACTTGAATTAATTAATGTCAGCAGATCAATCAAAAGT 915
Db 4361 CGGGAGGAGTTATGTTGATTTGACTATTTTCAAAAGGTCAGCAACCAATCAAAAGT 4420
QY 916 TATTTATTGAACAAGTCTTGTATTACTACGTTGTTGATTTAAACATGTAATTTCAAGAGG 975
Db 4421 TATTTGTTGAACAAGTATGTTATGTTATGTTTAAATTTAAGCATGTAATTTGAGAGG 4480
QY 976 ATAGTACTTTGATGTT 993
Db 4481 CTAGTACTTAGATGTT 4498

RESULT 11
US-10-723-947-90
; Sequence 90, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: Hordeum vulgare
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1105, 1156, 1190, 1197, 1209, 1237, 1238, 1239, 1240, 1241,

; -PRIOR FILING DATE: 2003-04-11
; -NUMBER OF SEQ ID NOS: 159
; -SOFTWARE: FastSeq for Windows Version 4.0
; -SEQ ID NO 84
; -LENGTH: 3454
; -TYPE: DNA
; -ORGANISM: Triticum dicoccoides
; -US-10-723-947-84

Query Match      32.2%; Score 320.8; DB 8; Length 3454;
Best Local Similarity 77.4%; Pred. No. 1.7e-82;
Matches 432; Conservative 0; Mismatches 62; Indels 64; Gaps 1;

QY 436 GTGCCATTTCCAGGAGTGCATTCAACAACACTATTAGCAATGAAGCAATCATGACTATT 495
Db 2645 GTGCCATTTCCGGGGCTGCATTCCACGACTATTAGCAATGAACGATCATGACTATT 2704
QY 496 GACACAGAGATGATGTGGGGCTGCCCATTTATCCACAATTCAGAGAGAGAGCGAAG 555
Db 2705 GATACAGAGATGATGTGGGGCTGCCCATTAATTCGACGATTCAGAGAGAGAGCGAAG 2764
QY 556 GTGATGAGGTATAGGAGAGAGAGAGAGAGCGCGCTATGACAAAGCAAAATCCGATACGAG 615
Db 2765 GTGATGAGGTATAGGAGAGAGAGAGAGAGCGCGTCTATGACAAAGCAAAATCCGCTATGAG 2824
QY 616 TCCAGAAAAGCTTACGCTGAGCTTCGGCCATCGGTCACGCGCGCTTTGTCAAGGTACCC 675
Db 2825 TCCAGAAAAGCTTACCGGAGCTTCAGGCAACGCTCAATGCGCGCTTTGTCAAGGTACCA 2884
QY 676 GAAGCCATGCGCATCATCTCCAGCTTCGCGCTATGATCCTTAGTAACTTCACCTC 735
Db 2885 GAAGCGCTGCTCGTCCGCTCAGCTTCGCGCTATGATCCTTAGTAACTTCACCTC 2944
QY 736 GGATGTTCCGGTAATTTATAGCACAGCCAGATAAAATGATAATTCCTCTGAT 795
Db 2945 GGATGTTCCGTAATTTATAGCACAGCCAGATAAAATGATAATTCCTCTGAT 2962
QY 796 TGATCCACCGTGAAGAGCAGTTGTTCTCTCAAAAGTAAATAGTCGGTTAGTATCGA 855
Db 2963 TGATCCACCGTGAAGAGCAGTTGTTCTCTCAAAAGTAAATAGTGGTTATGTTGACCGA 3000
QY 856 TTGGAGCCATTATGTTGACTTGAATTAATTAATGTCAGCAGATCAATCAAAAGT 915
Db 3001 TGGAGGAGGTATGTTGATTTGACTATTTCAAAAGGTCAGCAGATCAATCAAAAGT 3060
QY 916 TATTTATTGAACAAGTCTTGTATTACTACGTTGTTGATTTAAACATGTAATTTCAAGAGG 975
Db 3061 TATTTGTTGAACAAGTATGTTATGTTTAAATTTAAGCATGTAATTTGAGAGG 3120
QY 976 ATAGTACTTTGATGTT 993
Db 3121 CTAGTACTTAGATGTT 3138

RESULT 10
US-10-723-947-81
; Sequence 81, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 5734
```


RESULT 14

US-10-437-963-82314
; Sequence 82314, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 82314
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT MRT4530_81756C.1
US-10-437-963-82314

Query Match 8.6%; Score 86; DB 7; Length 1413;
Best Local Similarity 75.4%; Pred. No. 6.2e-14;
Matches .107; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
QY 540 GGAGAGAGCAGCGAAGGTGATGAGGTATAGGGAGAGAGAGAGAGAGCGCGGTATGACAA 599
DB 702 GGACCGGGAGCGAAGGTGCGGTACAGAGAGAGAGAGAGCGCGGTATGACAA 761
QY 600 GCAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGGCCG 659
DB 762 GCAGATCCGATACGCTCGCGAAGGCTACGCCGAGATCGCGCCCGCGGTGAAGGGCG 821
QY 660 CTTGTCAAGGTACCCGAGCC 681
DB 822 CTTGCCAAGGTGCGCCGACGGC 843

RESULT 15

US-09-938-842A-265
; Sequence 265, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 265
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-265

Query Match

7.7%; Score 76.6; DB 3; Length 885;

Best Local Similarity 62.1%; Pred. No. 2.8e-11;
Matches 121; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY 488 TGACTATTGACACAGAGATGATGGTGGGCGCTGCCCATTTATCCCAATGCGAGGAGAG 547
DB 629 TGACGGCGGAGATGACGAACACCGGAGACCCAGCTGTGCAGTTATCCCGCGGAGAGGG 688
QY 548 CAGCGAAGGTGATGAGGTATAGGGAGAGAGAGAGAGCGCGCTATGACAAAGCAAATCC 607
DB 689 AAGCAAGGGTTTTGAGGTATACAGAGAGAGAGAGAGAAATCGGAAATTTGAGAGAGCGATT 748
QY 608 GATACAGTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGCCCGCTTTGTCA 667
DB 749 GGTATGCGCTCGCGTAAAGCTTACGCTGAGATGAGCGCGAGAAATCAAAGGACGTTTGTCTA 808
QY 668 AGGTACCCCGAAGCCA 682
DB 809 AGAGAACAGATTCTGA 823

Search completed: February 23, 2006, 14:12:45
Job time : 995 secs

C	1	43.8	4.4	162013	12	US-11-150-688-30	Sequence 30, Appl
	2	43.6	4.4	200628	12	US-11-121-086-62	Sequence 62, Appl
	3	41.4	4.2	908	12	US-11-128-061-549	Sequence 549, App
	4	41.4	4.2	908	12	US-11-128-049-549	Sequence 549, App
	5	41.2	4.1	17263	8	US-10-995-561-13411	Sequence 13411, A
	6	41.2	4.1	93112	8	US-10-995-561-13234	Sequence 13234, A
C	7	41.2	4.1	105550	8	US-10-995-561-13235	Sequence 13235, A
	8	41	4.1	15544	12	US-11-010-239-112	Sequence 112, App
	9	40.8	4.1	7402	8	US-10-750-185-27313	Sequence 27313, A
	10	40.8	4.1	7402	8	US-10-750-623-27313	Sequence 27313, A
	11	40	4.0	565	6	US-09-925-065A-809991	Sequence 809991, A
C	12	40	4.0	659	6	US-09-925-065A-26496	Sequence 26496, A
C	13	39.8	4.0	628	6	US-09-925-065A-640012	Sequence 640012, A
C	14	39.6	4.0	60	12	US-11-136-527-7342	Sequence 7342, Ap
C	15	39.6	4.0	1428	12	US-11-136-527-3246	Sequence 3246, Ap
C	16	39.6	4.0	3924	8	US-10-750-185-24577	Sequence 24577, A
	17	39.6	4.0	3924	8	US-10-750-623-24577	Sequence 24577, A
C	18	39.4	4.0	1162	7	US-10-714-487-103	Sequence 103, App
C	19	39.4	4.0	114801	12	US-11-121-086-22	Sequence 22, Appl
C	20	39.2	3.9	150468	12	US-11-112-908-56	Sequence 56, Appl

;; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES

;; FILE REFERENCE: 09138.6000-00000

;; CURRENT APPLICATION NUMBER: US/11/121.086

;; CURRENT FILING DATE: 2005-05-04

;; PRIOR APPLICATION NUMBER: 60/567,570

;; PRIOR FILING DATE: 2004-05-04

;; NUMBER OF SEQ ID NOS: 107

;; SOFTWARE: Patentin version 3.3

;; SEQ ID NO 62

;; LENGTH: 200628

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-11-121-086-62

Query Match 4.4%; Score 43.6; DB 12; Length 200628;

Best Local Similarity 67.8%; Pred. No. 0.9;

Matches 61; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 166 CCATTCACCATCATCATCACCATCATCAGGACGAGTGTGTGAGTACCATGTTCTTC 225

DB 129584 CACCATCATCATCATCACCATCATCACCACCATCATCATCATCATCATCATCAT 129643

QY 226 GCCATGGCAACACACACACACACCAT 255

DB 129644 CACCATCATCATCATCACCACCATCAT 129673

RESULT 3

US-11-128-061-549

;; Sequence 549, Application US/11/128061

;; Publication No. US20060003958A1

;; GENERAL INFORMATION:

;; APPLICANT: Charlebois, Timothy S.

;; APPLICANT: Mounts, William M.

;; APPLICANT: Hann, Louane E.

;; APPLICANT: Sinacore, Martin S.

;; APPLICANT: Leonard, Mark W.

;; APPLICANT: Brown, Eugene L.

;; APPLICANT: Miller, Christopher P.

;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS

;; FILE REFERENCE: 01997.027701

;; CURRENT APPLICATION NUMBER: US/11/128,061

;; CURRENT FILING DATE: 2005-05-11

;; PRIOR APPLICATION NUMBER: US 60/570,425

;; PRIOR FILING DATE: 2004-05-11

;; NUMBER OF SEQ ID NOS: 7285

;; SOFTWARE: Patentin version 3.3

;; SEQ ID NO 549

;; LENGTH: 908

;; TYPE: DNA

;; ORGANISM: Cricetulus sp.

;; FEATURE:

;; NAME/KEY: misc_feature

;; LOCATION: (29)..(45)

;; OTHER INFORMATION: n is a, c, g, or t

US-11-128-061-549

Query Match 4.2%; Score 41.4; DB 12; Length 908;

Best Local Similarity 57.3%; Pred. No. 0.32;

Matches 75; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 174 CCATCATCATCATCATCAGGACGAGTGTGTGAGTACCATGTTCTTCGCCCATGG 233

DB 58 CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 117

QY 234 CAACACACACACACACCATGGCTGGGAGCAGACTACCCAGTCCACCCGCCGCGCAGA 293

DB 118 CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 117

QY 294 CAACTTCGACC 304

DB 178 CAAACCCCATC 188

DB 178 CAAACCCCATC 188

RESULT 4

US-11-128-049-549

;; Sequence 549, Application US/11/128049

;; Publication No. US20060010513A1

;; GENERAL INFORMATION:

;; APPLICANT: Melville, Mark W.

;; APPLICANT: Mounts, William M.

;; APPLICANT: Hann, Louane E.

;; APPLICANT: Sinacore, Martin S.

;; APPLICANT: Leonard, Mark W.

;; APPLICANT: Brown, Eugene L.

;; APPLICANT: Miller, Christopher P.

;; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR

;; FILE REFERENCE: 01997.027700

;; CURRENT APPLICATION NUMBER: US/11/128,049

;; CURRENT FILING DATE: 2005-05-11

;; PRIOR APPLICATION NUMBER: US 60/570,425

;; PRIOR FILING DATE: 2004-05-11

;; NUMBER OF SEQ ID NOS: 7285

;; SOFTWARE: Patentin version 3.3

;; SEQ ID NO 549

;; LENGTH: 908

;; TYPE: DNA

;; ORGANISM: Cricetulus sp.

;; FEATURE:

;; NAME/KEY: misc_feature

;; LOCATION: (29)..(45)

;; OTHER INFORMATION: n is a, c, g, or t

US-11-128-049-549

Query Match 4.2%; Score 41.4; DB 12; Length 908;

Best Local Similarity 57.3%; Pred. No. 0.32;

Matches 75; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 174 CCATCATCATCATCATCAGGACGAGTGTGTGAGTACCATGTTCTTCGCCCATGG 233

DB 58 CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 117

QY 234 CAACACACACACACACCATGGCTGGGAGCAGACTACCCAGTCCACCCGCCGCGCAGA 293

DB 118 CCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCA 117

QY 294 CAACTTCGACC 304

DB 178 CAAACCCCATC 188

RESULT 5

US-10-995-561-13411

;; Sequence 13411, Application US/10995561

;; Publication No. US2005027054A1

;; GENERAL INFORMATION:

;; APPLICANT: CARGILL, Michele et al.

;; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

;; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

;; FILE REFERENCE: CL001559

;; CURRENT APPLICATION NUMBER: US/10/995,561

;; CURRENT FILING DATE: 2004-11-24

;; NUMBER OF SEQ ID NOS: 85702

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 13411

;; LENGTH: 17263

;; TYPE: DNA

;; ORGANISM: Homo sapiens

US-10-995-561-13411

Query Match 4.1%; Score 41.2; DB 8; Length 17263;

Best Local Similarity 52.3%; Pred. No. 1.4; DB 8; Length 105550;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 126 TTGTGCGGCGCAACAATGCGCGCTCATGTCTCGCCCATTCACCATCATCA 185
Db 10017 TTGGTTCTGTCAATAATATCATCAACCATCTCTTCACTGCGCACTATGGCCATCATCA 10076
QY 186 CCATCATCAGGAGCACAGCTGTGTGAGTACCACTTCTTCGCCCATGGCAACCAACCA 245
Db 10077 CTACCACTCCACATCAACCTGCCATCATCATCAACGATCATCAACCAACCACTA 10136
QY 246 CCACCACTATGGTGGCGAGCACTACCCAGTGCCACCGCCGCCAGACAATT 299
Db 10137 CCATTATCCACCATCAACCACTAGAGTTATTACTACCATCACTACAACCAATT 10190

RESULT 6

US-10-995-561-13234
; Sequence 13234, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13234
; LENGTH: 93112
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(93112)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-995-561-13234

Query Match 4.1%; Score 41.2; DB 8; Length 93112;
Best Local Similarity 64.9%; Pred. No. 2.9;
Matches 61; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 161 TCTGCGCCATTACCATCATCATCACTACCATCATCAGGAGCAGCAGCTGTGTGAGTACCA 220
Db 83559 TCACCACTACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 83618
QY 221 TCTTGGCCCATGGCAACCAACCAACCAACCAACCA 254
Db 83619 ACACCATCATCATCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 83652

RESULT 7

US-10-995-561-13235/c
; Sequence 13235, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13235
; LENGTH: 105550
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13235

Query Match 4.1%; Score 41.2; DB 8; Length 105550;
Best Local Similarity 52.3%; Pred. No. 3.1; DB 8; Length 105550;
Matches 91; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 126 TTGTGCGGCGCAACAATGCGCGCTCATGTCTCGCCCATTCACCATCATCA 185
Db 1028 TTGGTTCTGTCAATAATATCATCAACCATCTCTTCACTGCGCACTATGGCCATCATCA 969
QY 186 CCATCATCAGGAGCACAGCTGTGTGAGTACCACTTCTTCGCCCATGGCAACCAACCA 245
Db 969 CTACCACTCCACATCAACCTGCCATCATCATCAACGATCATCAACCAACCACTA 909
QY 246 CCACCACTATGGTGGCGAGCACTACCCAGTGCCACCGCCGCCAGACAATT 299
Db 908 CCATTATCCACCATCAACCACTAGAGTTATTACTACCATCACTACAACCAATT 855

RESULT 8

US-11-010-239-112
; Sequence 112, Application US/11010239
; Publication No. US20060015970A1
; GENERAL INFORMATION:
; APPLICANT: ROGER PENNELL
; APPLICANT: JACK OKAMURO
; APPLICANT: RICHARD SCHNEEBERGER
; APPLICANT: YIWEN FANG
; APPLICANT: SHING KWOK
; APPLICANT: DIANE JOFUKU
; APPLICANT: EDWARD A. KIEGLE
; APPLICANT: JONATHAN DONSON
; APPLICANT: NESTOR APUYA
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES ENCODED THEREBY USEFUL FOR
; TITLE OF INVENTION: MODIFYING PLANT CHARACTERISTICS
; FILE REFERENCE: 2750-1585PUS2
; CURRENT APPLICATION NUMBER: US/11/010,239
; CURRENT FILING DATE: 2004-12-09
; PRIOR APPLICATION NUMBER: US 60/529,352
; PRIOR FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: Patent version 3.3
; SEQ ID NO 112
; LENGTH: 1544
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1544)
; OTHER INFORMATION: 12600234_construct_ID_YP0279
US-11-010-239-112

Query Match 4.1%; Score 41; DB 12; Length 1544;
Best Local Similarity 56.2%; Pred. No. 0.53;
Matches 77; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 543 GAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGGAGGAGCGCGCTATGCAAGCA 602
Db 1146 GCGAGAGCAAGTGTGAGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1205
QY 603 AATCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTCAACGCGCGCTT 662
Db 1206 AATTCGATACCAAGTTCCAAAACCTCAATCTGATCAACGCTCTCGAATGAAGGAGCA 1265
QY 663 TGTCAAGGTACCGAAG 679
Db 1266 CGTGAGAGGCGCAATG 1282

RESULT 9

US-10-750-185-27313
; Sequence 27313, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.

APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-2
CURRENT APPLICATION NUMBER: US/10/750,185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27313
LENGTH: 7402
TYPE: DNA
ORGANISM: Bovine 19866880890824
US-10-750-185-27313

Query Match 4.1%; Score 40.8; DB 8; Length 7402;
Best Local Similarity 67.9%; Pred. No. 1.2;
Matches 57; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 172 CACATCATCATCACCACCATCAGGACACAGCTGTGAGTACCAAGTTCTTCGGCCAT 231
DB 1968 CACATCATCATCACCACCATCACCACCATCACCACCATCACCACCATCCTCTAT 2027

QY 232 GGCAACACACACACACACCAT 255
DB 2028 CATGACACACATCACCACCATCAT 2051

RESULT 10
US-10-750-623-27313
Sequence 27313, Application US/10750623
Publication No. US20050287531A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM1100-1
CURRENT APPLICATION NUMBER: US/10/750,623
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437,482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64922
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27313
LENGTH: 7402
TYPE: DNA
ORGANISM: Bovine 19866880890824
US-10-750-623-27313

Query Match 4.1%; Score 40.8; DB 8; Length 7402;
Best Local Similarity 67.9%; Pred. No. 1.2;
Matches 57; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 172 CACATCATCATCACCACCATCAGGACACAGCTGTGAGTACCAAGTTCTTCGGCCAT 231
DB 1968 CACATCATCATCACCACCATCACCACCATCACCACCATCACCACCATCCTCTAT 2027

QY 232 GGCAACACACACACACACCAT 255
DB 2028 CATGACACACATCACCACCATCAT 2051

RESULT 11

US-09-925-065A-809991
Sequence 809991, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 809991
LENGTH: 565
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-809991

Query Match 4.0%; Score 40; DB 6; Length 565;
Best Local Similarity 51.9%; Pred. No. 0.63;
Matches 111; Conservative 1; Mismatches 101; Indels 1; Gaps 1;

QY 138 CAACAACTGCGCGCCTCATGCTCTCGCCCATTTACCATCATCATCATCATCAGGA 197
DB 12 CCATCACACACACCGTCACTACAACTGCCCCCTCCACCATCATCATCATCATCCTCCA 71

QY 198 GCACCAAGCTGTGTAGTACCA-GTTCTTGGCCCATGGCAACCAACCAACCAACCATG 256
DB 72 CCAGCACACAGCAGCGGCACCACTATACAGCCACCACTTACACCTTCAACCAACCAAC 131

QY 257 GCTCGCAGCAGACATACCCAGTGCCACCGCCGACCACTTTCGACCAACCAACCAACAT 316
DB 132 AGTAGTACCGTCACTACAAACCAACCACTTCCACGACCAACATTCATCACCAGCTCCAT 191

QY 317 GGACCAAGACATTTTCATGAACACAGCAGCGCAGG 350
DB 192 GGTTAGCCTTCTCTTCTTAACACAGCAGGAAG 225

RESULT 12
US-09-925-065A-26496/c
Sequence 26496, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26496

```
; LENGTH: 659
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-26496

Query Match
  4.0%; Score 40; DB 6; Length 659;
Best Local Similarity 62.2%; Pred. No. 0.68;
Matches 61; Conservative 1; Mismatches 36; Indels 0; Gaps 0;

QY 157 ATGGTCTCCCATTCACCATCATCATCAGGAGCAGGAGTGTGTGAGTAC 216
Db 130 ATCTTCTTCTTGAACCAACCATCATTCACCAACCAACCAACCAACCAAC 71
QY 217 CAGTTCTTCGCGCATGCGCAACCAACCAACCAACCAACCAACCA 254
Db 70 CACCACCACTACCAACCAACCAACCAACCAACCAACCAACCAACCA 33

RESULT 13
US-09-925-065A-640012/c
; Sequence 640012, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 640012
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-640012

Query Match
  4.0%; Score 39.8; DB 6; Length 628;
Best Local Similarity 67.5%; Pred. No. 0.76;
Matches 56; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 172 CACCATCATCATCACCATCATCAGGAGCAGGAGTGTGTGAGTACCACTTCTTCGCCCAT 231
Db 270 CACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 211
QY 232 GGCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 254
Db 210 CACCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 188

RESULT 14
US-11-136-527-7342/c
; Sequence 7342, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26

; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3246
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3246/c
; Sequence 3246, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3246
; LENGTH: 1428
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3246

Query Match
  4.0%; Score 39.6; DB 12; Length 1428;
Best Local Similarity 63.8%; Pred. No. 1.2;
Matches 60; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 162 CTCGCCCATTCACCATCATCATCAGGAGCAGGAGCAGGAGTGTGTGAGTACCACTT 221
Db 1320 CACACACATACATCATCATCATCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAG 1261
QY 222 CTCGCCCATTCACCATCATCATCAGGAGCAGGAGCAGGAGCAGGAGCAGGAGCAGGAG 255
Db 1260 CCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCA 433

Search completed: February 23, 2006, 12:15:03
Job time : 406 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2006, 11:04:50 ; Search time 810 Seconds

(without alignments)
1909.103 Million cell updates/sec

Title: US-10-723-947-77

Perfect score: 1048

Sequence: 1 MSMSGCLGCANNCPLMVSP.....YESRKAYALPRVNGRFVK 187

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Q=/abss/ABSSWEB_spool/US10723947/runat_23022006_085407_16435/app_query.fasta_1
-DB=Published Applications NA Main -QFMT=fastap -SUPFIX=p2n.rnpbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1
-MATRIX=blosum62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03p
-USER=US10723947 @CGN 1 1 1549 @runat_23022006_085407_16435 -NCPU=6 -ICPU=3.
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DEPOP=6 -DELEXT=7

Database : Published Applications NA_Main:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1035	98.8	996	US-10-723-947-75	Sequence 75, Appl
2	907.5	86.6	975	US-10-723-947-79	Sequence 79, Appl
3	816	77.9	7051	US-10-723-947-74	Sequence 74, Appl
4	768.5	73.3	639	US-10-723-947-88	Sequence 88, Appl
5	756	72.1	642	US-10-723-947-91	Sequence 91, Appl
6	730.5	69.7	639	US-10-723-947-82	Sequence 82, Appl
7	729.5	69.6	639	US-10-723-947-85	Sequence 85, Appl

8	670.5	64.0	2913	8	US-10-723-947-78	Sequence 78, Appl
9	590	56.3	1985	8	US-10-723-947-87	Sequence 87, Appl
10	572.5	54.6	2043	8	US-10-723-947-90	Sequence 90, Appl
11	547.5	52.2	5734	8	US-10-723-947-81	Sequence 81, Appl
12	538	51.3	3454	8	US-10-723-947-84	Sequence 84, Appl
13	258	24.6	864	7	US-10-437-963-83163	Sequence 83163, A
14	237	22.6	901	8	US-10-425-115-34955	Sequence 34955, A
15	232.5	22.2	1413	7	US-10-437-963-82314	Sequence 82314, A
16	207	19.8	1297	3	US-09-770-445-17	Sequence 17, Appl
17	207	19.8	1370	7	US-10-425-114-14597	Sequence 14597, A
18	207	19.8	1404	7	US-10-425-114-13058	Sequence 13058, A
19	204	19.5	972	7	US-10-767-701-11858	Sequence 11858, A
20	194	18.5	1320	7	US-10-437-963-25736	Sequence 25736, A
21	192	18.3	1768	7	US-10-437-963-40	Sequence 40, Appl
22	189.5	18.1	1385	7	US-10-425-114-26389	Sequence 26389, A
23	189.5	18.1	1633	8	US-10-425-115-157740	Sequence 157740, A
24	188	17.9	1101	5	US-10-143-849-7	Sequence 7, Appl
25	186.5	17.8	872	7	US-10-767-701-13864	Sequence 13864, A
26	185.5	17.7	577	7	US-10-260-238-390	Sequence 390, App
27	184.5	17.6	742	8	US-10-425-115-157736	Sequence 157736, A
28	184.5	17.6	1441	8	US-10-739-930-5473	Sequence 5473, Ap
29	181.5	17.3	1396	7	US-10-767-701-12421	Sequence 12421, A
30	180.5	17.2	1101	5	US-10-143-849-5	Sequence 5, Appl
31	180	17.2	698	7	US-10-425-114-14609	Sequence 14609, A
32	180	17.2	1202	7	US-10-425-114-20132	Sequence 20132, A
33	180	17.2	1553	7	US-10-425-114-8013	Sequence 8013, Ap
34	180	17.2	1593	8	US-10-739-930-325	Sequence 225, App
35	179.5	17.1	1139	7	US-10-437-963-101201	Sequence 101201, A
36	177.5	16.9	1415	7	US-10-424-599-33981	Sequence 33981, A
37	176.5	16.8	596	7	US-10-021-323-14874	Sequence 14874, A
38	176.5	16.8	885	3	US-09-938-842A-265	Sequence 265, App
39	176.5	16.8	885	3	US-09-938-842A-265	Sequence 265, App
40	176.5	16.8	1002	7	US-10-280-238-403	Sequence 403, App
41	176.5	16.8	1075	7	US-10-425-114-22406	Sequence 22406, A
42	176.5	16.8	1120	7	US-10-412-699B-597	Sequence 597, App
43	176.5	16.8	1141	5	US-10-295-403-107	Sequence 107, App
44	176.5	16.8	2717	7	US-10-437-963-30197	Sequence 30197, A
45	175	16.7	1124	5	US-10-143-849-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-10-723-947-75
; Sequence 75, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION AND USES THEREOF
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Triticum monococcum
US-10-723-947-75

Alignment Scores:

Pred. No.: 1.56e-111 Length: 996
Score: 1035.00 Matches: 185
Percent Similarity: 99.5% Conservative: 1
Best Local Similarity: 98.9% Mismatches: 1
Query Match: 98.8% Indels: 0
DB: 8 Gaps: 0


```
US-10-723-947-77 (1-187) x US-10-723-947-74 (1-7051)
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 3001 ATGTCATCATCATCGGTTTGTGCGCGCGCAACACTGCGCGGCTCATGCTCGCGCC 3060
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
DB 3061 ATTCACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 3120
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 60
DB 3121 CATGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 3180
QY 61 ProAspAsnPheAspHisArgArgThrThrThrThrThrThrThrThrThrThrThrThr 80
DB 3181 CCAGACAACTTGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 3240
QY 81 GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlyGlyGlyGlyGlyGly 100
DB 3241 GGGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3300
QY 101 ValGlnProProAlaAlaHisHisHisHisHisHisHisHisHisHisHisHisHisHis 109
DB 3301 GTGCAGCCACCGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 3360
QY 109 ----- 109
DB 3361 TTGCCGATGATGCGTCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3420
QY 109 ----- 109
DB 3421 TGACTACACCCACTACAAAAGAGTACCAACATGTAACCAATTCATATATTTCTCACATTA 3480
QY 109 ----- 109
DB 3481 TTCTGTAAATTTACGCTGCTCGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 3540
QY 109 ----- 109
DB 3541 ATATTCTTTAATTTCTATGGAGCATAGATTTGTGTTTGTATTTAGTTGATGAGAAT 3600
QY 109 ----- 109
DB 3601 TGTATGGGTTGCAAAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 3660
QY 109 ----- 109
DB 3661 AAGAAGGTAATCAGTCATACATGCATCTGAAAAATTTAGACTTGTGTGCAATAAATACTA 3720
QY 109 ----- 109
DB 3721 ACCAACTCGACCGGCACAGCTGGGGAAGACTTTAATCAAGCTGTAGCTAGAGCTTAAT 3780
QY 109 ----- 109
DB 3781 AATATACATATCTCTTTATGGATCAAGCAATACATATATGCGCTCAATTTCTCACTTGTG 3840
QY 109 ----- 109
DB 3841 AATATCTATCTGGAGTCCACACTTTATGTAATTAATTCACAAAGTTTGTGAAATGGAC 3900
QY 109 ----- 109
DB 3901 AATATACATCTGGATCGATGCACCCTTTTCTCATTTTATGTGGTCAATTAATTAATGATT 3960
QY 109 ----- 109
DB 3961 GTTATTTAGTATTTCAATTTTATCTGACGTAGTTTTTGCAAGCTGTGACTCATATATAA 4020
QY 109 ----- 109
DB 4021 CTGATACTACTCCCAAGATAGCTTGGTAGTGGCGGGGTGATCGATCTACCGAGTTTCAAT 4080

QY 109 ----- 109
DB 4081 AAAACTGATCGAGATCGGGTCCAAAAAAGAAACAAACCCATACAAAATGGAAGAAGATCC 4140
QY 109 ----- 109
DB 4141 TTGTTTAGTTAGTTTGGCATCAGAAAATTCGCTAAATTAGTTACTTGTGATCAATCTTTTGA 4200
QY 109 ----- 109
DB 4201 ACATGSCATGTTTACCCCAACGAGCCAGATCAACAATTAATGTAAGATTAGCGCTTTT 4260
QY 109 ----- 109
DB 4261 AAAAATCTATAAACTGTACATACATGTACAGGGGTACACATGTACATATAACACCTA 4320
QY 109 ----- 109
DB 4321 ATTAACAGTATATTTGTAGACCAATTGATTTTGACGCTGGCATCTTTTGAAAAAATAA 4380
QY 109 ----- 109
DB 4381 TGCCAGAGAGTTGTTAGCTTCCACTGTCCAGAAATAGAATAGTTACAAATCAAGTGCATC 4440
QY 109 ----- 109
DB 4441 TCTGAATGAAATGSGATCATTTTCTAGTTAATTAGAGACCAATTAGATACTTTCATAAACA 4500
QY 109 ----- 109
DB 4501 GGGAGATATCAAGTACGTATCTGTACCATAAAGAAAGTACATAAATCGGATCTTATGAT 4560
QY 110 -----ValProPheTyrGlyAlaPheThrAsnThrIleSer 122
DB 4561 TATTTTCTCTGTGTTTCAGGTGCCATTTCCAGGAGTGCATTCACCAACTATTATAG 4620
QY 123 AsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThr 142
DB 4621 AATGAGCAATCATGATCATTTTGACACAGAGATGATGGTGGGCGCTGCCCATTTATCCACA 4680
QY 143 MetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgArgTyr 162
DB 4681 ATGCAGGAGAGAGCAGCAGCAAGGTGATGAGGTATATGGAGAGAGAGAGAGAGCGGCTAT 4740
QY 163 AspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsn 182
DB 4741 GACAAGCAAAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGGCCATGGGTC AAC 4800

QY 183 GlyArgPheValLys 187
DB 4801 GGCCGCTTTGTCAAG 4815

RESULT 4
US-10-723-947-88
; Sequence 88, Application US/10723947
; Publication No. US20040205948A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 639
; TYPE: DNA
```

ORGANISM: Hordeum vulgare
US-10-723-947-88

Alignment Scores:
Pred. No.: 2,086-80 Length: 639
Score: 756.50 Matches: 148
Percent Similarity: 82.6% Conservatives: 9
Best Local Similarity: 77.9% Mismatches: 28
Query Match: 73.3% Indels: 5
DB: 8 Gaps: 3

US-10-723-947-77 (1-187) x US-10-723-947-88 (1-639)

```
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 1 ATGTCATGTGTCATGTCGCGCGCCAGCAATGCGGTACACATGATGTCGCC 60
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
DB 61 GTTCTTCTTCATCATCACCATCATCAGGAACACCCACTGCACGAGTACCA 120
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 59
DB 121 CAAGGT-----CACACACACACACACAGCGCGGCGGAGGACTACCC 174
QY 60 ProProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79
DB 175 CGCCAGACAAATGCGCCACACACACATCATGACCAACCGCGCTTTCATGA 234
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
DB 235 CCAGAGAACAGACCAACAGGCTCACACGGGAGGTGGACGCGCGGCCCAAC 294
QY 100 LeuValGlnProProAla-----ArgAlaHisIleValProPheTyrGlyGlyAlaPhe 117
DB 295 CTGCTCGACCCACCGCGCGCCGCGCAAGACCAACCATCTGTCGCATTCG 354
QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetValGlyPro 137
DB 355 GCCAGCACTATTAGCAACGACGATCATGCTATTGATACAGAAATGATGGT 414
QY 138 AlaHisTyrProThrMetGlnGluArgAlaAlaIleValMetArgTyrArgGluLysArg 157
DB 415 GCCTATATCCACAGATGCAGGAGAGAGAGAGGCGGAAGGTGATGAGGT 474
QY 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
DB 475 AAGAGCGCGGCTATGACAGCAAAATCCGCTACGAGTCCAGAAAGCTTAC 534
QY 178 ArgProArgValAsnGlyArgPheValLys 187
DB 535 AGCCACGGGTCAATGCGCGCTTTGCAAG 564
```

RESULT 5

US-10-723-947-91

Sequence 91, Application US/10723947
Publication No. US20040205848A1

GENERAL INFORMATION:

APPLICANT: Dubcovsky, Jorge

APPLICANT: Yan, Liuling

APPLICANT: Loukianov, Artem

TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION

TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF

FILE REFERENCE: 514112000320

CURRENT APPLICATION NUMBER: US/10/723,947

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: US 10/412,137

PRIOR FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 159

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 91

LENGTH: 642

TYPE: DNA

ORGANISM: Hordeum vulgare
US-10-723-947-91

Alignment Scores:
Pred. No.: 6,218-79 Length: 642
Score: 756.00 Matches: 146
Percent Similarity: 82.6% Conservatives: 11
Best Local Similarity: 76.8% Mismatches: 29
Query Match: 72.1% Indels: 4
DB: 8 Gaps: 3

US-10-723-947-77 (1-187) x US-10-723-947-91 (1-642)

```
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 1 ATGTCATGTGTCATGTCGCGCGCCAGCAATGCGGTATGCGGTATCACA 60
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
DB 61 GTTCTTCTTCATCATCACCATCATCAGGAACATCGGACGCGGAGTACCA 120
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 59
DB 121 CAAGGT---CACACACACACACACAGCGCGGCGGAGGACTACCC 177
QY 60 ProProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79
DB 178 CGCCGCGCAATGCGCCACACGAGATCATGCGGCCACGCTGTTTCATGA 237
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
DB 238 CCAGTGAATAGCACAGGCTCACACAAGAGGTGGACGCGCGGCCCAAC 297
QY 100 LeuValGlnProProAla-----ArgAlaHisIleValProPheTyrGlyGlyAlaPhe 117
DB 298 CTGCTCGACCCACCGCGCGCCGCGCAAGACCAACCATCTGTCGCATTC 357
QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetValGlyPro 137
DB 358 ACCAACACTATTAGCAACGACGATCATGCTATTGATACAGAGATGATG 417
QY 138 AlaHisTyrProThrMetGlnGluArgAlaAlaIleValMetArgTyrArgGluLysArg 157
DB 418 GCCTATATCCACAGATGCAGGAGAGAGAGGCGGAAGGTGATGAGGT 477
QY 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
DB 478 AAGAGCGCGGCTATGACAGCAAAATCCGCTACGAGTCCAGAAAGCTT 537
QY 178 ArgProArgValAsnGlyArgPheValLys 187
DB 538 AGCCACGGGTCAACGCGCGCTTTGCAAG 567
```

RESULT 6

US-10-723-947-82

Sequence 82, Application US/10723947
Publication No. US20040205848A1

GENERAL INFORMATION:

APPLICANT: Dubcovsky, Jorge

APPLICANT: Yan, Liuling

APPLICANT: Loukianov, Artem

TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION

TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF

FILE REFERENCE: 514112000320

CURRENT APPLICATION NUMBER: US/10/723,947

CURRENT FILING DATE: 2003-11-26

PRIOR APPLICATION NUMBER: US 10/412,137

PRIOR FILING DATE: 2003-04-11

NUMBER OF SEQ ID NOS: 159

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 82

LENGTH: 639

TYPE: DNA

ORGANISM: Triticum monococcum
US-10-723-947-82

Alignment Scores:

Pred. No.: 6,21e-76 Length: 639
Score: 730.50 Matches: 144
Percent Similarity: 81.6% Conservative: 11
Best Local Similarity: 75.8% Mismatches: 28
Query Match: 69.7% Indels: 7
DB: 8 Gaps: 4

US-10-723-947-77 (1-187) x US-10-723-947-82 (1-639)

```
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 1 ARGTCATGTCATGCGGTTTGTGCGGCGCAAGCGACTGCCCGCACCACATGATCTCGCCC 60
QY 21 IleHisHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPheAla 40
DB 61 GTT-----CTTCAGCATCAGGACACACACTGCGTGGCGAGTACCAGTTCTTCACC 111
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60
DB 112 CAAGGC---CACCAACCACACACACCGCGCGCGGCGGACTTACCACCGCCACCGCCA 168
QY 61 ProAsp---AsnPheAspHisArgArgThrTTPThrArgProPheHisGluThrAlaAla 79
DB 169 CCGTGGCGCAATGCCACCACTGCAGATCATGGACCAACCCGCTTTCATGAAACAGCAGCT 228
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
DB 229 GCAGGGAACAGCAGCAGACTCAGCTGGAGGTAGTAGCGCGCGCCCAACATGGCTCAC 288
QY 100 LeuValGlnProProAlaAlaAlaHis-----IleValProPheTyrGlyGlyAlaPhe 117
DB 289 CTGCTGCAGCCACCGCGCACCGCAAGAACCAACCACTCGTCCATCTTCGCGGGGCTGCATTC 348
QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
DB 349 ACCAGCATATTAGCAATGCACAAATCATGACTATTGTATACAGAGATGATGGTGGGGCT 408
QY 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157
DB 409 GCCCATTAATCTGACGATGCAGGAGAGAGAGCGGAGGTAAGGTATGAGGTACAGGAGAGAGG 468
QY 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
DB 469 AAGAGCGGTGCTATGACAAGCAAAATCCGCTACGAGTCCAGAAAAGCTTACGCCGAGCTC 528
QY 178 ArgProArgValAsnGlyArgPheValLys 187
DB 529 AGGCCACGGGTCAATGGCTTTGTCAAG 558
```

RESULT 7

US-10-723-947-85

; Sequence 85, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; FILE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 639
; TYPE: DNA

ORGANISM: Triticum dicoccoides
US-10-723-947-85

Alignment Scores:

Pred. No.: 8,15e-76 Length: 639
Score: 729.50 Matches: 143
Percent Similarity: 81.6% Conservative: 12
Best Local Similarity: 75.3% Mismatches: 28
Query Match: 69.6% Indels: 7
DB: 8 Gaps: 4

US-10-723-947-77 (1-187) x US-10-723-947-85 (1-639)

```
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 1 ARGCCCATGTCATGCGGTTTGTGCGGCGCAAGCGACTGCCCGCACCACATGATCTCGCCC 60
QY 21 IleHisHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPheAla 40
DB 61 GTT-----CTTCAGCATCAGGACACACACTGCGTGGCGAGTACCAGTTCTTCACC 111
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60
DB 112 CAAGGC---CACCAACCACACACACCGCGCGGCGGACTTACCACCGCCACCGCCA 168
QY 61 ProAsp---AsnPheAspHisArgArgThrTTPThrArgProPheHisGluThrAlaAla 79
DB 169 CCGTGGCGCAATGCCACCACTGCAGATCATGGACCAACCCGCTTTCATGAAACAGCAGCT 228
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
DB 229 GCAGGGAACAGCAGCAGGCTCAGCTGGAGGTAGTAGCGCGCGCCCAACATGGCTCAC 288
QY 100 LeuValGlnProProAlaAlaAlaHis-----IleValProPheTyrGlyGlyAlaPhe 117
DB 289 CTGCTGCAGCCACCGCGCACCGCAAGAACCAACCACTCGTCCATCTTCGCGGGGCTGCATTC 348
QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
DB 349 ACCAGCATATTAGCAATGCACAAATCATGACTATTGTATACAGAGATGATGGTGGGGCT 408
QY 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157
DB 409 GCCCATTAATCTGACGATGCAGGAGAGAGAGCGGAGGTAAGGTATGAGGTACAGGAGAGAGG 468
QY 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
DB 469 AAGAGCGGTGCTATGACAAGCAAAATCCGCTATGAGTCCAGAAAAGCTTACGCCGAGCTC 528
QY 178 ArgProArgValAsnGlyArgPheValLys 187
DB 529 AGGCCACGGGTCAATGGCGCTTTGTCAAG 558
```

RESULT 8

US-10-723-947-78

; Sequence 78, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; FILE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 2913
; TYPE: DNA

ORGANISM: Triticum dicoccoides
US-10-723-947-78

Alignment Scores:
Pred. No.: 5,32e-68 Length: 2913
Score: 670.50 Matches: 168
Percent Similarity: 28.3% Conservative: 3
Best Local Similarity: 27.8% Mismatches: 9
Query Match: 64.0% Indels: 424
DB: 8 Gaps: 2

US-10-723-947-77 (1-187) x US-10-723-947-78 (1-2913)

```
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 578 ATGTCATGTCATGCGGTTGTGCGGGCCCAACAACATGCGCGGCTCATGTCGCGCC 637
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
DB 638 ATTTCATCGTCATCACCATCATCAGGAGCAGCAGCTGCTCAGCAGCAGCTTCTTCGCG 697
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 60
DB 698 CAAAGGCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 736
QY 61 ProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAlaAla 80
DB 737 CCAGCCAACTTCGACCATAGCAAGACATGACCAACATTCATGAAACAGCAGCTGCA 796
QY 81 GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlyGlyGlyGlyGlyGly 100
DB 797 GGGAAACAGCAGCAGGCTCAGCTGGAGGTGGGGCGAGCGGCGGCGGCGGCGGCGGCGG 856
QY 101 ValGlnProProAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 109
DB 857 GTGACGCCACCGGCAAGAGCCCAATCATGTAAGTAGTAGTACCGCTTAATGTTTCAATCTC 916
QY 109 ----- 109
DB 917 TTGCCGATGGATCGTCCCTGGGCTCTCTCTTAAATAATCCCACTTAATTTATGTCATCTC 976
QY 109 ----- 109
DB 977 TATACCCACTACAAAAAATAGCACCATGTAAACATCTCATATATCTGTGCAGATAATCT 1036
QY 109 ----- 109
DB 1037 GTTAATGTACGCTCAATTTGTTCTCTGAAAAAGATATGGCGGGAATGGATCTTGATAT 1096
QY 109 ----- 109
DB 1097 TCTTTAATTTCTATGGAGCATATATAGATTTTGTGTTTGTATTAGTTGATGCAGAT 1156
QY 109 ----- 109
DB 1157 TGTATGGGTTGCAAAATCATCATCATATATAAACTTATTTCATTTTATTGACCAAC 1216
QY 109 ----- 109
DB 1217 AACAGGTAATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 1276
QY 109 ----- 109
DB 1277 ACTCGAGCGGCAGCTGGGGAGAGACTTTAATCAAGCTGCTAGCTAGAGCTTAATAATA 1336
QY 109 ----- 109
DB 1337 TAACATATCTCTTTATGGGATCAAGCAATACATATGCGCTCAATTTCTCAACTTGTCAATA 1396
QY 109 ----- 109
DB 1397 TCTATCTGGAGTCCACACTTTATGGTAATTAATGTGACAAAGTTTGTGAAATGGACAATA 1456
```

```
QY 109 ----- 109
DB 1457 TACATACTGGATCGATGCACCCCTTTTCTCATTTTATGTGGTCATTATGAATTTGATTGT 1516
QY 109 ----- 109
DB 1517 TATTTAGTATTCAATTTTATCTTGAGCTAGTTTTCGAAGTCTGTAGCTCATATATAACT 1576
QY 109 ----- 109
DB 1577 GATACTACTCCCAACGATAGCTTGGCTAGTGGCGGGTGCATCGATCTACCGAGTTTCATAA 1636
QY 109 ----- 109
DB 1637 AACTGATCGAGATCGGTCCAAAAAAGAAACCAACCAACCAACCAACCAACCAACCAACCA 1696
QY 109 ----- 109
DB 1697 GTTTAGTTAGTTTGCATCAGAAAAATGGCTAATTAGTTACTTGTCTATCAATCTTTTGAAC 1756
QY 109 ----- 109
DB 1757 ATGGCATGTTACCCCCAACCGACTCAGATCACAATTTATTGATGAAGTTACGCTTTTAA 1816
QY 109 ----- 109
DB 1817 AACTCATAAAACTGTACATACATGTACAGGGCTACACACATGTACATATACACCTAAT 1876
QY 109 ----- 109
DB 1877 TAAAAAGTATATTCGTAGACCAATTTGTTTGGACGGTGCACATCTTTGAAAAAATATGCC 1936
QY 109 ----- 109
DB 1937 AGAGGAGTTGTAGCTTCCACTGTCCAGAAATAGTAATAGTTACAATCAAGTGCATCTCTG 1996
QY 109 ----- 109
DB 1997 AATGAAATGGATCATTTTCTAGTTAATTAGAGACCAATTAGATACTTCAATAACAGGGG 2056
QY 109 ----- 109
DB 2057 AGTATCAAGTAGTATCTGTCTACCTCAAGAAAGTACATACTGCGATCTTATGATTATTT 2116
QY 110 -----ValProPheThrGlyAlaPheThrAsnThrIleSerAsnG 124
DB 2117 TCCTCTTCATGTTTCAGGTGCCATTTTACGAGGTGCATTCACCAACACATATTAGCAATGA 2176
QY 124 uAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisIleThrProThrMetG 144
DB 2177 AGCAATCATGACTATTGACACAGAGATGATGTTGGGGCTGCCCATTTATCCCAACATGCA 2236
QY 144 nGluArgAlaAlaIleValMetArgTyrArgGluIleValArgIleValArgIleValArg 164
DB 2237 GGAGAGACAGCGAAGGTGATGAGGTATAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2296
QY 164 sGlnIleArgTyrGluSerArgIleAlaIleAlaIleAlaIleAlaIleAlaIleAlaIle 184
DB 2297 GCAATCATGATACGATCCAGAAAGCTTACGCTGAGCTTCGCGCCACCGGCTCAACCGCTG 2356
QY 184 gPheValIle 187
DB 2357 CTTTGTCAAG 2366
```

RESULT 9

US-10-723-947-87
; Sequence 87, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION

; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF

```

; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87
; LENGTH: 1985
; TYPE: DNA
; ORGANISM: Hordeum vulgare
US-10-723-947-87

Alignment Scores:
Pred. No.:          9.68e-59          Length: 1985
Score:             590.00             Matches: 147
Percent Similarity: 29.6%             Conservative: 9
Best Local Similarity: 27.9%           Mismatches: 29
Query Match:       56.3%              Indels: 342
DB:                8                 Gaps: 4

US-10-723-947-77 (1-187) x US-10-723-947-87 (1-1985)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 336 ATGTCCATGTCATGTGGTTGTGGCGCGCCAGCACTTCGGCGTACCACATGATGTGCGCC 395
QY 21 IleHisHisHisHisHisHisHisHisGlnLeuHisGlnLeuCysGlyTyrGlnPhePheAla 40
DB 396 GTTCTTCTTCATCATCATCACTCATCATCGAAGAACCCCACTGCGACGAGTACCAGTTCTTCGCC 455
QY 41 HisGlyAsnHisHisHisHisHisHisHisGlySerAlaalaasptYr---ProValProPro 59
DB 456 CAAGGT-----CACCAACCAACCAACGAGCGCGGAGGACTACCCACCAACCAACCGCCA 509
QY 60 ProProAspAsnPheAspHisAsArgThrTriThrArgProPheHisGluThrAlaAla 79
DB 510 CCGCCGACAAATGCCACCAACCAACAGATCATGGACCAACCGCGTTTCATGAACACAGCAGCT 569
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
DB 570 CCAGAGAACACAGCACAGGCTCACACGGGAGGTGGACGCGCGGCCAACACATGGCTCAC 629
QY 100 LeuValGlnProProAla----- 105
DB 630 CTGCTGCAGCCACCGCGCGCCGCAAGAGCCACCATCGTGAGTAGTACTACTGTTAAATTT 689
QY 105 ----- 105
DB 690 TTCTATCTCTTGGCGATCGATGGGACCTGCTAACAAAAATCACACTTTCTTAATTTCCAT 749
QY 105 ----- 105
DB 750 CTCAAAAAAGACTACGCCCATGTGACCAGCTCATATATATATATATATATATATATATATAT 809
QY 105 ----- 105
DB 810 TATTCCTGGTCGATTTGTAATTTTACCAAGCGAGAAAGCTTGTAATTTGTATCAGTTGATGCA 869
QY 105 ----- 105
DB 870 CAAGAATGGCGGCTCACGTCATCAGTCGCACATACTATATATATATATATATATATATATTTGA 929
QY 105 ----- 105
DB 930 CTAAACAAGTAACTAGTTAAATTCCTTTATGGGTCAGCAACATATATATATATATATATATAT 989
QY 105 ----- 105
DB 990 ATGTTAATTCCTTGACAAAGTTTGTGAAGTGGAAAAATATATATTTACTTTTATCAATGCACCT 1049
QY 105 ----- 105

```

```

; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 2043
; TYPE: DNA
; ORGANISM: Hordeum vulgare
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1105, 1156, 1190, 1197, 1209, 1237, 1238, 1239, 1240, 1241,
; LOCATION: 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251,
; LOCATION: 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261,
; LOCATION: 1262, 1263, 1264, 1265, 1294, 1300, 1313, 1326, 1340
; OTHER INFORMATION: n = A, T, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1359, 1385
; OTHER INFORMATION: n = A, T, C or G
US-10-723-947-90

Alignment Scores:
Pred. No.: 1,16e-56 Length: 2043
Score: 572.50 Matches: 146
Percent Similarity: 30.3% Conservative: 11
Best Local Similarity: 28.2% Mismatches: 29
Query Match: 54.6% Indels: 332
DB: 8 Gaps: 4

US-10-723-947-77 (1-187) x US-10-723-947-90 (1-2043)
QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 420 ATGTCATGCGATCGCGTGTGTGCGCGCGAGCAATTTGCCGCTATCACATGATGTCGCC 479
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
DB 480 GTTCTTCTCATCATCACCATCATCAGACATCATCGGCGCGAGTACCAGTCTTTCGCC 539
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 59
DB 540 CRAAGGT--CACCACCACCACCACCACCGCGCGCGAGCAGCTACCCACCGCCACAGCCA 596
QY 60 ProProAspAsnPhaeAspHisArgArgThrTyrThrArgProPheHisGluThrAlaAla 79
DB 597 CGCCCGCGCAATTTGCCACCACCGCAGATCATCGGCCACCGCTGTTCATGAAACAGAGCT 656
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlyGlyGlyGlyGlyGly 99
DB 657 CCACTGAATAGCACCGAGGCTCACACAGAGGTGGACGCGCGGCCACACAGATGGCTCAC 716
QY 100 LeuValGlnProProAla-Arg----- 106
DB 717 CTGCTGCAGCACCGCGCGCGCCAGAGCCACCATCGTGAGTACTACTGCTTAATCGTTC 776
QY 106 ----- 106
DB 777 CATCTCTCCCGATCGATGTGACTCCTCTTAACAAAATACACTTTCTTAATTTCCATC 836
QY 106 ----- 106
DB 837 TCAAAAAAGCTAGCGCCATGTGACCAGCTCATATATCTGTACATAAATCCGCTTAATT 896
QY 106 ----- 106
DB 897 ATGCTGCTCGATTGTAATTTACCAAGCAGCAAGATTGTGTTTGTATCATGTTGATGCAC 956
QY 106 ----- 106
DB 957 AAGACTGGATGCTCAGATCATCATGACATACATATATATATTTTATTTTATTTGAC 1016
QY 106 ----- 106
DB 1017 TAACAAGGTAATCAGTTAATTCCTTTTATGGGGTCAAGCAACATATGTCACGCCCTCATG 1076

QY 106 ----- 106
DB 1077 TTAATTCCTTGGCAGAGTTTGTGAAATANAAGATATATATTTGGATCAATGCACCTACC 1136
QY 106 ----- 106
DB 1137 TCTTTCTCATTTTATGTGNGCATTTTAAAAATTTGAATGCTATTTTGTATTTAATTTCTC 1196
QY 106 ----- 106
DB 1197 NTGAGCTAGTTGNGAAGCTTATAGCTCAATTTAACTGGAANNNNNNNNNNNNNNNNNN 1256
QY 106 ----- 106
DB 1257 NNNNNNNCGAGTTTCATGAAACTGATCAAGATCAGTNCAAAANAGGCCAACCTCNCGA 1316
QY 106 ----- 106
DB 1317 AATGGAATTCGATCCTTGTTAANTAGTTTGCATCAGGAATNGGCTACTTAACTACTTG 1376
QY 106 ----- 106
DB 1377 CTACCAATTTTATGAAGATGGCATGTTCTCTCAAAATGATGATCCAGCTCACAATTTTGG 1436
QY 106 ----- 106
DB 1437 TGAAGTTAAACATTTTATAGCAATTCATAAAGGTGCATAGATGTACAGGGGTACACGTAC 1496
QY 107 ----Alahis----- 108
DB 1497 ACACGCACATATATACGCTAGTTAAACATATATGATAGACAAATGAGTTTGGCAAT 1556
QY 108 ----- 108
DB 1557 GCGCTTCTTGGACATATGCGCGGAAATTTCTCTCTTCCATTCTCTAAAAACATAGA 1616
QY 108 ----- 108
DB 1617 ACAGTTAGAAATCAAGTGCAACCACTGAATGAGAATGGGTCAATTTTGGTTAACGAGAC 1676
QY 109 -----11eVa 110
DB 1677 CACTATAGTTTATAAACACTGTACTCTCTCACCATTGTTTCTCTCGATGTTTCAGGT 1736
QY 110 lProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAs 130
DB 1737 GCCATTCGCGCGAGTGCAATTCACCAACACTATTAGCAACGCAACGATCATGACTATTGA 1796
QY 130 pThrGluMetMetValGlyProAlaHisTyrProThrMetGlnGluAlaAlaAlaAlaVa 150
DB 1797 TACAGAGATGATGCGCGGAGCTGCTTATAGTCCACGATGCAGGAAGAGAGCAAAAGT 1856
QY 150 lMetArgTyrArgGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGlyAlaGly 170
DB 1857 GATGAGTACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1916
QY 170 rArglyValatyrAlaGluLeuArgProArgValAsnGlyArgPheVallys 187
DB 1917 CAGAAAAGCTTACGCGCGAGCTTAGGCCACGGGTCAACGGCGCTTTGTCAAG 1968

RESULT 11
US-10-723-947-81
; Sequence 81, Application US/10723947
; Publication NO. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcoveky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukoianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 514112000320
; CURRENT APPLICATION NUMBER: US/10/723,947
```

```
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: US 10/412,137
; PRIOR FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 5734
; TYPE: DNA
; ORGANISM: Triticum monococcum
US-10-723-947-81

Alignment Scores:
Pred. No.: 3,95e-53 Length: 5734
Score: 547.50 Matches: 145
Percent Similarity: 28.2% Conservatives: 11
Best Local Similarity: 26.2% Mismatches: 27
Query Match: 52.2% Indels: 371
DB: 8 Gaps: 5

US-10-723-947-77 (1-187) x US-10-723-947-81 (1-5734)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 2589 ATGTCATGTCATGCGGTTTGTGCGCGCAAGGACTGCCCGCACCACCATGATCTCGCC 2648
QY 21 IleHisHisHisHisHisHisHisHisGlnGlnLeuCysGlnTyrGlnPhePheAla 40
DB 2649 GTT-----CTTCAGCATCAGGACACACATGGCTGGCGGAGTACCAGTTCTTCACC 2699
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro 60
DB 2700 CAAGGC---CACCACCACCACCACCACCGCGCGCGGAGCTACCCACCGCCACGCCA 2756
QY 61 ProAsp---AsnPhaAspHisArgArgThrTrpThrArgProPheHisGlnThrAlaAla 79
DB 2757 CCGTCGCGCAATTGCCACCACCTCCAGATCATGACGACACACACCGCTTTCATGAAACAGCAGCT 2816
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
DB 2817 GCAGGGAACAGACGACAGATCAGCTGGAGTAGATGACGGCGGCCCAAAACATGGCTCAC 2876
QY 100 LeuValGlnProProAlaArg----- 106
DB 2877 CTGCTGACGCCACCGCCACGCGCAAGAACACCACCATCGTGAGTAGTACTACTGCTTAATTG 2936
QY 106 ----- 106
DB 2937 TTCCAGCTCTTGCCGATCGCTGGGGCTCTCTTGTAACAAAAGTTCCCTTTTACGTAATCT 2996
QY 106 ----- 106
DB 2997 CCATCTACTCCCCCCCCCCCCCCCCCCCCCCCCCGCCCGCCCTCCCGCATCTCAAAAAAGT 3056
QY 107 -----AlaHisIle----- 109
DB 3057 TAGCGCCATGTAACAGCTCATATATCTGTGCATATATCTGTTAATTATGCTGCTCAA 3116
QY 109 ----- 109
DB 3117 TTATATCTCCCAAGCAGGAAGTTGTGTTTGTATCATGTTGATGAACAAGAATGGGAA 3176
QY 109 ----- 109
DB 3177 CTCACATCATCAGTTACACATACATATCTATTTTCATTTTATTTGACAAAGGTAATCA 3236
QY 109 ----- 109
DB 3237 GTTAATTCCTTTTATGGGAACAAGACATACATATGTCCAGCCTTCATGTTAATTCCTTGA 3296
QY 109 ----- 109
DB 3297 CAAAGTTTGTGAAATGGCAATATATATCTGGATCAATGACCCCTCTTCTCATTTTAT 3356
```

```
QY 109 ----- 109
DB 3357 GTGGTCATTTATGAATTTTAGTGCTATTTATATATTTAAATTTCTCTTAAGCTTGTTTG 3416
QY 109 ----- 109
DB 3417 TAAGCTTATAGCTCATGTATACAGATACACTACTCCCAATAATGTCTCGTAGTGCCGG 3476
QY 109 ----- 109
DB 3477 GTGATCAATCTACCGAGTTTCATAAAACCTGATCGGATCAGATCCAAAAACAGACAAACC 3536
QY 109 ----- 109
DB 3537 TCACGAAATAGAAACAAGATCTCTTTGTTAATTAAGTTTGACCAGGAAATGGCTACTTAA 3596
QY 109 ----- 109
DB 3597 TTACTTTCTATCAATCTTATGAACATGGCATGTTTCTCACATATGGTGACCCAGATCACA 3656
QY 109 ----- 109
DB 3657 ATTGTGACGAGTTAAACATTTTAGCAATTCATAAAACCATGACAGATGTACAGGC 3716
QY 109 ----- 109
DB 3717 TAGCGTATGCACATACATATACACCTAATTAACATATATTCATAGAGCATTTGAGT 3776
QY 109 ----- 109
DB 3777 TTGGACTGTGCGCTTCTTTGGACACAAAGGCCCGGAGTGTCTCTTCCATTTGCTAG 3836
QY 109 ----- 109
DB 3837 AAAAATAGAACAGTTACATCAATCAAGTGACCACTGAATGAATAATGGGTCAACTCTGGTTAA 3896
QY 109 ----- 109
DB 3897 TAAGAGACCACTGTACTTTCATAAACAGGGAATATCATGTACATATCTGCAACCCACAG 3956
QY 110 -----ValProPheTyr 113
DB 3957 AAAAGTACAGAGCTGCACCTCTTACAGTTATTTTCTCTTTCATGTTTCAGGTGCCATTTGC 4016
QY 114 GlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMet 133
DB 4017 GGGGTGCTATTCACCGACACTATTAGCAATCAACAATCATGACTATTGATACAGAGATG 4076
QY 134 MetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyr 153
DB 4077 ATGGTGGGGCTGCCCTAATCTGAGATGACAGGAGAGAGAGCGGAGGTGATGAGGTAC 4136
QY 154 ArgGlyLysArgLysArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAla 173
DB 4137 AGGGAGAAAGAGAGAGCGGTGCTATGACAGCAAAATCCGCTACGAGTCCAGAAAAGCT 4196
QY 174 TyrAlaGluLeuArgProArgValAsnGlyArgPheValLys 187
DB 4197 TAGCCGAGCTCAGGCCCGGCTCAATGCTCTTGTCAAG 4238

RESULT 12
US-10-723-947-84
; Sequence 84, Application US/10723947
; Publication No. US20040205848A1
; GENERAL INFORMATION:
; APPLICANT: Dubcovsky, Jorge
; APPLICANT: Yan, Liuling
; APPLICANT: Loukianov, Artem
; TITLE OF INVENTION: GENES RESPONSIBLE FOR VERNALIZATION
; TITLE OF INVENTION: REGULATION IN TEMPERATE GRASSES AND USES THEREOF
; FILE REFERENCE: 51411200320
; CURRENT APPLICATION NUMBER: US/10/723,947
; CURRENT FILING DATE: 2003-11-26
```


;; PRIOR APPLICATION NUMBER: US 10/412,137
;; PRIOR FILING DATE: 2003-04-11
;; NUMBER OF SEQ ID NOS: 159
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 84
;; LENGTH: 3454
;; TYPE: DNA
;; ORGANISM: Triticum dicoccoides
US-10-723-947-84

Alignment Scores:

Pred. No.: 2,66e-52 Length: 3454
Score: 538.00 Matches: 145
Percent Similarity: 28.5% Conservative: 12
Best Local Similarity: 26.4% Mismatches: 26
Query Match: 51.3% Indels: 367
DB: 8 Gaps: 5

US-10-723-947-77 (1-187) x US-10-723-947-84 (1-3454)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 1243 ATGCCATGTCATGGGTTGTGGCGGCGAAGGACTGCCCGCACCATGATCTCGCCC 1302
QY 21 IleHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPheAla 40
DB 1303 GTT-----CTTCAGCATCAGGAACACACCGGCTGGCGAGTACCACTTCTTCACC 1353
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60
DB 1354 CAAAGC---CACCAACACACACACACGAGCGGCGGAGTACCGCCGCCCGCCCA 1410
QY 61 ProAsp---AsnPheAspHisArgThrTriThrArgProPheHisGluThrAlaAla 79
DB 1411 CCGTCAGCAATTGCCACCACTCCAGATCATGACACACCGTTTCATGAACAGCAGCT 1470
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
DB 1471 GCAGGGAACAGCAGCAGGCTCAGCTGGAGGTAGACGCGCGCCCAAAACATGGCTCAC 1530
QY 100 LeuValGlnProProAlaArg----- 106
DB 1531 CTGCTGACGACCGGACGCGCCCAAGAACACCAACCATCGTGAGTAGTACTACTGCTTAATG 1590
QY 106----- 106
DB 1591 TTCCAGCTCTTGGCGATCGCTTGGCGCTCCTTCTAACAAAAGTTCCTTTTACGTAATCT 1650
QY 106----- 106
DB 1651 CCATCTACTCCCCCCCCCCCCCCCCCGGCATCTCAAAAAAAGTTAGCGCCATGTAACC 1710
QY 107 -AlaHisIle----- 109
DB 1711 AGCTCATATATCTGTCAGTAATCTGTTAATTATGCTGGTTGAATATAATCTCCCAAG 1770
QY 109----- 109
DB 1771 GCAGAGTGTGTGTTTGTGTTGTGTCAGTTGTCACAGAAGATGGGCACTCACATCATCAGTT 1830
QY 109----- 109
DB 1831 ACACATACATCTTAATTTTCAATTTTATTTGACTAACCAAGGTAATCAGTTAATCTCTTATG 1890
QY 109----- 109
DB 1891 GGAACAAGCAATACATATGTCCACGCTTCATGTTAATTCCTTGACAAAGTTTGGAAT 1950
QY 109----- 109
DB 1951 GGCAATATATATCTGGATCAGTCAGCCACCATCTTTTTCATTTTATGTTGGTCATTTATGA 2010
QY 109----- 109

DB 2011 TTTTAGTGCTATTTTGTATTTAAATTTTCTCTTAAGCTTGTGTTTGTAAAGCTTATAGCTC 2070
QY 109----- 109
DB 2071 AAGTATACAGATACACTACTCTCCCAATAATGCTTCGCTAGTGGCGGGTGATCAATCTACC 2130
QY 109----- 109
DB 2131 GAGTTTCAAAAACTGATCGAAATCAGATCCAAAAACAGACCAAAACCTCAGAAATAGAAA 2190
QY 109----- 109
DB 2191 CAAGATCCCTGTTTAATTAAGTTTGACACAGSAAATTTGCCTACTTAATTAATTTCTATCAA 2250
QY 109----- 109
DB 2251 TCTTATGAAGATGGTATGTTTCTCAGATATGGTGATCCAGATCACAATTTGTTGACGGAGT 2310
QY 109----- 109
DB 2311 TAAACATTTTGTAGCAATTCATAAACCGGTGCACAGATGTACAGGGCTACCGGTATGCACA 2370
QY 109----- 109
DB 2371 TACATAATACACCTAATTTAAACATATATTCATAGAGCGATTGAGTTTGGACTGTGGCT 2430
QY 109----- 109
DB 2431 TCTTTGGACAAAGGCCCGGGAAGTTGTTCTCTTCCATTGTCTAGAAAAATAGAACAGT 2490
QY 109----- 109
DB 2491 TACAATCAAGTGCACCACTGAATGAAATGGGTCAATTCTGTGTTAATAAGAGACCAACTG 2550
QY 109----- 109
DB 2551 TACTTCATAAACAGGGAATATCATGTATATCTGCAACCCACAGAGAAAGTACAGAACT 2610
QY 110-----ValProPheTyrGlyAlaPheTh 118
DB 2611 GCACCTTACGATTATTTTCTCTTTCATGTTTCAGGTGCCATTCGCGGGCTCATTCAC 2670
QY 118 rAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAl 138
DB 2671 CAGCACTATTAGCAATGCAACGATCATGACTATTGATACAGAGATGATGTTGGGGCTGC 2730
QY 138 aHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLy 158
DB 2731 CCATAATCTGACGATGCGAGGAGAGAGCGGAAGGTGATGAGGTACAGGAGAGAGAGAA 2790
QY 158 sArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuAr 178
DB 2791 GAGCGGTGCTATGACAGCAATTCGCTATCAGTCCAGAAAAGCTTACCGGAGCTCAG 2850
QY 178 gProArgValAsnGlyArgPheValLys 187
DB 2851 GCCACGGGTCAATGCCCGCTTTGTCAAG 2878

RESULT 13

US-10-437-83163
; Sequence 83163, Application US/10437963
; Publication NO. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barzakuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 83163

; LENGTH: 864

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_82521C.1

US-10-437-963-83163

Alignment Scores:
Pred. No.: 4,016-20 Length: 864
Score: 258.00 Matches: 84
Percent Similarity: 40.6% Conservative: 19
Best Local Similarity: 33.1% Mismatches: 61
Query Match: 24.6% Indels: 90
DB: 7 Gaps: 14

US-10-723-947-77 (1-187) x US-10-437-963-83163 (1-864)

```
QY 1 MetSerMet-----SerCysGlyLeuCysGlyAlaAsnAsn-----12
DB 91 ATGTCGATGGGACACGACCGGAGNAGATGTGGCTGTGGCGCCGACGGTGGCGGC 150
QY 13 ---CysProArgLeuMetValSerProLeuHisHisHisHisHisGlnGluHis 31
DB 151 TGTGTGTCCTCCGC-----CATCGCCACGATGATGAT 180
QY 32 -----GlnLeuCys-----34
DB 181 GGATTCCTTCGTCTTCCCGCGAGTGTGGTCCAGGGGATCGCGCCCGCGGCACACG 240
QY 35 -----GluTyrGlnPhePheAlaHisGlyAsnHisHisHisHisHisGlySerAla 52
DB 241 GTGCACGAGTTCAGTCTTC-----GGCAGCAGCGGCGGCGGCGGCGGAGC 294
QY 53 Ala-----AspTyrProValProProPro-----ProAspAsnPhe 64
DB 295 GTGGCTGGCTGTTCGATGACTACCGCGCGCGTGTGCTGCTGCGCGCGCGGATG 354
QY 65 AspHisArgArgThrTrpThrArgProPhe-----CGTACGACGCGCGTGTG 405
DB 355 CATCATCGGCACCG-----CGTACGACGCGCGTGTGCGCGCGCGCGTGTGTC 405
QY 75 ---HisGluThrAlaAlaAlaGlyAsnSerSerArgLeuThrLeuGluVal-----90
DB 406 AGAGGAACACCGCGCGCGCGG-----CTCAGTTGACGTCTCCCTCGCGC 453
QY 91 -----GlyAlaGlyGlyGlnHisMetAla 98
DB 454 GAACGCCCGACCTGGACCGCGGCTCGCGCTCGCGCGCGCGCGCGCGCGCGC 507
QY 99 HisLeuValGlnProProAlaArgAlaHisIleValProPheTyrGlyAlaPheThr 118
DB 508 -----GCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 561
QY 119 AsnThrIleSerAsn-----GluAlaIleMetThrIleAspThrGluMet 133
DB 562 GACGACGCGCGCTCGATGTCACGAGGAGATGTTGGCGCGCGCGCGCGCGCG 621
QY 134 MetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyr 153
DB 622 TTGAACCCAAACACCGGTGTGGCGCAATGTTGGAGAGGAGGAGGAGGAGGAG 681
QY 154 ArgGluLysArgLysArgArgTyrAspLysGlnIleArgTyrGlnSerArgLysAla 173
DB 682 AAGGAGAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 741
QY 174 TyrAlaGluLeuArgProArgValAsnGlyArgPheValLys 187
```

DB 742 TATGCCGAGATGAGGCCCGGAGTGAGAGGTGCTTTCGCCAAA 783

RESULT 14

US-10-425-115-34955

; Sequence 34955, Application US/10425115

; Publication No. US20040214272A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 369326

; SEQ ID NO 34955

; LENGTH: 901

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: MRT4577_131881C.1

US-10-425-115-34955

Alignment Scores:
Pred. No.: 1,268-17 Length: 901
Score: 237.00 Matches: 67
Percent Similarity: 42.5% Conservative: 21
Best Local Similarity: 32.4% Mismatches: 55
Query Match: 22.6% Indels: 64
DB: 8 Gaps: 8

US-10-723-947-77 (1-187) x US-10-425-115-34955 (1-901)

```
QY 22 HisHisHisHisHisHisGlnGlnHisGln-----32
DB 326 CACCAACACACACACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 385
QY 33 -----LeuCysGluTyrGlnPhePheAlaHisGlyAsnHisHis-----45
DB 386 GCGCGCGCGCTGCAGGAGTTCAGTTCTTCGCCACGACGACGACGACGACG 445
QY 46 -----HisHisHisHisGly-----SerAlaAla 53
DB 446 TGGCTGTTCACAGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 505
QY 54 AspTyrProValPro-----ProProProAspAsnPheAspHis 66
DB 506 AACGGGGTGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 565
QY 67 ArgArgThrTrpThrArgProPheHisGlu-----ThrAlaAla 79
DB 566 GCTCAGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 625
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGlu-----ValGlyAla 92
DB 626 GCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 685
QY 93 GlyGlyGlnHisMetAlaHisLeuValGlnProProAlaArgAlaHisIleValProPhe 112
DB 686 GCGGACAGCAATCCAGCG-----ACGACGTCCCGCGCGCGCGCGCGCG 733
QY 113 TyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGlu 132
DB 734 TCGCGGAGCAGCGTTTTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 793
QY 133 MetMetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArg 152
DB 794 GTG-----GACCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 820
QY 153 TyrArgGluLysArgLysArgArgTyrAspLysGlnIleArgTyrGluSerArgLys 172
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2006, 10:42:28 ; Search time 183 Seconds
(without alignments)
1816.415 Million cell updates/sec

Title: US-10-723-947-77

Perfect score: 1048

Sequence: 1 MSMSGCLGANNCPRLMVSP.....YESRKAYAEIPLRVNGRFVK 187

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -DEV=xlh

-Q=/abs/ABSSWEB/spool/US10723947/runat_23022006_085401_16267/app_query.fasta_1
-DB=Issued Patents NA -QFMT=fastap -SUFFIX=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs07 -USER=US10723947 @CGN 1 1 193 @runat_23022006_085401_16267
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA..

1: /cgn2_6/prodata/1/ina/1 COMB.seq.*
2: /cgn2_6/prodata/1/ina/5 COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B COMB.seq.*
5: /cgn2_6/prodata/1/ina/6C COMB.seq.*
6: /cgn2_6/prodata/1/ina/6CTUS COMB.seq.*
7: /cgn2_6/prodata/1/ina/PP COMB.seq.*
8: /cgn2_6/prodata/1/ina/RE COMB.seq.*
9: /cgn2_6/prodata/1/ina/baGkfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	17.9	1101	3	US-08-945-056-7
2	180.5	17.2	1101	3	US-08-945-056-5
3	175	16.7	1124	3	US-08-945-056-1
4	170	16.2	4201	3	US-08-945-056-4
5	161	15.4	448	3	US-09-640-211A-327
6	132	12.6	72549	3	US-09-949-016-16477
7	130	12.4	25603	3	US-09-819-607-3
8	129	12.3	39154	3	US-09-949-016-12384
9	129	12.3	39154	3	US-09-949-016-12801

c 10	129	12.3	39443	3	US-09-949-016-14326	Sequence 14326, A
c 11	129	12.3	39443	3	US-09-949-016-14327	Sequence 14327, A
c 12	127.5	12.2	67620	3	US-09-949-016-16939	Sequence 16939, A
c 13	126.5	12.1	152132	3	US-09-949-016-13845	Sequence 13845, A
c 14	126.5	12.1	152145	3	US-09-949-016-12371	Sequence 12371, A
c 15	126	12.0	55195	3	US-09-949-016-15854	Sequence 15854, A
c 16	126	12.0	142783	3	US-09-949-016-15127	Sequence 15127, A
c 17	124.5	11.9	18596	3	US-09-318-448-11	Sequence 11, Appl
c 18	124.5	11.9	18596	3	US-09-577-268-11	Sequence 11, Appl
c 19	124.5	11.9	18597	3	US-09-962-665-8	Sequence 8, Appl
c 20	124.5	11.9	18597	3	US-09-963-333-8	Sequence 8, Appl
c 21	124.5	11.9	18597	3	US-09-962-677-8	Sequence 20, Appl
c 22	123.5	11.8	3563	3	US-09-041-886-20	Sequence 5, Appl
c 23	123.5	11.8	3596	2	US-08-779-801-5	Sequence 5, Appl
c 24	123.5	11.8	3596	2	US-09-298-441-5	Sequence 3, Appl
c 25	123.5	11.8	3632	2	US-08-779-801-3	Sequence 3, Appl
c 26	123.5	11.8	3632	2	US-08-779-801-4	Sequence 3, Appl
c 27	123.5	11.8	3632	2	US-09-298-441-3	Sequence 4, Appl
c 28	123.5	11.8	3632	3	US-09-298-441-4	Sequence 4, Appl
c 29	123.5	11.8	7808	2	US-08-149-097D-22	Sequence 22, Appl
c 30	123.5	11.8	7808	3	US-08-949-386-22	Sequence 22, Appl
c 31	123.5	11.8	7808	3	US-08-450-562-22	Sequence 22, Appl
c 32	123.5	11.8	7808	3	US-08-984-709A-22	Sequence 22, Appl
c 33	123.5	11.8	7808	3	US-08-450-272-22	Sequence 22, Appl
c 34	123.5	11.8	7808	3	US-08-450-273-22	Sequence 22, Appl
c 35	123.5	11.8	7815	3	US-09-949-016-3629	Sequence 3629, Ap
c 36	123.5	11.8	7815	3	US-09-949-016-3630	Sequence 3630, Ap
c 37	123.5	11.8	34230	3	US-09-949-016-12052	Sequence 12052, A
c 38	123.5	11.8	128470	3	US-09-949-016-13765	Sequence 13765, A
c 39	122.5	11.7	840	3	US-09-248-796A-4756	Sequence 4756, Ap
c 40	121.5	11.6	1853	2	US-08-553-110-2	Sequence 2, Appl
c 41	121.5	11.6	4168	3	US-09-266-225D-17	Sequence 17, Appl
c 42	121.5	11.6	4279	3	US-09-041-886-22	Sequence 22, Appl
c 43	121	11.5	209	3	US-09-513-999C-14394	Sequence 14394, A
c 44	120.5	11.5	3680	2	US-08-759-848-1	Sequence 1, Appl
c 45	120.5	11.5	3680	6	PCT-US95-09383-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-08-945-056-7
; Sequence 7, Application US/08945056
; Patent No. 6077994
; GENERAL INFORMATION:
; APPLICANT: Coupland, George M.
; APPLICANT: Putterill, Joanna J.
; TITLE OF INVENTION: Genetic control of flowering
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye PC
; STREET: 8th Floor, 1100 No. 6077994th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,056
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02561
; FILING DATE: 01-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422083.7
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ms Mary J Wilbon
; REGISTRATION NUMBER: 32,955

Db 682 ATCACTATGGCTCTCCAGCAATGCTCTACCAACCAATGGTTCCATAAACCATACGCA 741
Qy 101 ValGlnProAlaArgAlaHisIleValProPheTyGlyGlyAlaPheThrAsnThr 120
Db 742 TACAATCCATCAATGGAAGTGAAGTCTGTGTCGCG--GAGCAGACAGCACTGCACAAACA 798
Qy 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro--AlaHis 139
Db 799 GTTTCATCTCCAAAACGCAAGGAGAGATAGAAAACCTCCTGAACCTCTTAATTCAG 858
Qy 140 TyrProMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArg 159
Db 859 ATTCTCAGTCCATGACAGAGAGAGCTAGAGCTCTGAGATACAGAGAGAGAGAGAGA 918
Qy 160 ArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgPro 179
Db 919 AGAAGTCTTGAAGAGACAATAGGTATGCTTCAAGGAAGGCATATGCAGAGAGAGAGCG 978
Qy 180 ArgValAsnGlyArgPheValLys 187
Db 979 AGGATCAATGGACGGTTTGCAGAG 1002

RESULT 3

US-08-945-056-1
; Sequence 1, Application US/08945056
; Patent No. 6077994
; GENERAL INFORMATION:
; APPLICANT: Coupland, George M.
; APPLICANT: Putterill, Joanna J.
; TITLE OF INVENTION: Genetic control of flowering
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vandervhye PC
; STREET: 8th Floor, 1100 No. 6077994th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,056
; FILING DATE: 20-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/02561
; FILING DATE: 01-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9422083.7
; FILING DATE: 02-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ms Mary J Wilson
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 620-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; STRAIN: Landsberg erecta
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: chromosome 5

FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1119
; US-08-945-056-1
Alignment Scores:
Pred. No.: 1.82e-08 Length: 1124
Score: 175.00 Matches: 51
Percent Similarity: 40.9% Conservative: 25
Best Local Similarity: 27.4% Mismatches: 56
Query Match: 16.7% Indels: 54
DB: 3 Gaps: 5

US-10-723-947-77 (1-187) x US-08-945-056-1 (1-1124)

Qy 9 GlyAlaAsnAsnCyProArgLeuMetValSerProIleHisHisHisHisHisHis 28
Db 625 GGGGAGATAGAGTGTGTTCCGCTTAACCTTAAGAAATCAAGGGGCCACCAGTGCCCAAC 684
Qy 29 GlnGluHisGlnLeuCysGluTyrGlnPheAlaHisGlyAsnHisHisHisHis 45
Db 685 CAACAGAATTTTCAGTTCAATATCAATATGCTCTCAGGAGACTCCTACACGCAAT 744
Qy 46 -----HisHisHisGlySerAlaAlaAspTyrProValProProPro 61
Db 745 GTTTCATTAACCATACGATACATATTCATCCATGGAACCTGTTGTCGCG----- 798
Qy 62 AspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAlaGly 81
Db 799 -----GAGTCAACAGCATGTGTGCACA 819
Qy 82 AsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHisLeuVal 101
Db 820 ACAGCTTTCACCCCAAGAACGCCCAAGGAGCAGTAGAGCAA----- 861
Qy 102 GlnProProAlaArgAlaHisIleValProPheTyrGlyAlaPheThrAsnThrIle 121
Db 862 CAACCTGACCTCGCAAGCCAGATGATA----- 888
Qy 122 SerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrPro 141
Db 889 -----ACAGTAACACCAACTCAGTCCA----- 909
Qy 142 ThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgArg 161
Db 910 -----ATGGACAGAGAACCCAGGCTCTGAGATACAGAGAGAGAGAGAGAGAA 963
Qy 162 TyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgVal 181
Db 964 TTTGAGAGACATAAGGTATGCTTCCAGGAAGGCATATGCAGAGATAAGCCGGGTC 1023
Qy 182 AsnGlyArgPheValLys 187
Db 1024 AATGGCCGTTTCGCAAG 1041

RESULT 4

US-08-945-056-4
; Sequence 4, Application US/08945056
; Patent No. 6077994
; GENERAL INFORMATION:
; APPLICANT: Coupland, George M.
; APPLICANT: Putterill, Joanna J.
; TITLE OF INVENTION: Genetic control of flowering
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vandervhye PC
; STREET: 8th Floor, 1100 No. 6077994th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible


```

; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15854
; LENGTH: 55195
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15854

```

Alignment Scores:	0.363	Length:	55195
Pred. No.:	126.00	Matches:	21
Score:	61.5%	Conservative:	3
Percent Similarity:	53.8%	Mismatches:	14
Best Local Similarity:	12.0%	Indels:	2
Query Match:	3	Gaps:	1
DB:			

US-10-723-947-77 (1-187) x US-09-949-016-15854 (1-55195)

[illegible]

Search completed: February 23, 2006, 12:01:53
Job time : 221 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2006, 10:39:32 ; Search time 3661 Seconds
(without alignments)
2389.835 Million cell updates/sec

Title: US-10-723-947-77

Perfect score: 1048

Sequence: 1 MMSCLCGANNCPLMVSP.....YESRKAYAEPRVNGRFRVK 187

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-O=/abes/ABSSWEB.spool/US10723947/runat_23022006_085359_16224/app_query.fasta_1
-DB=EST -OPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abes02h
-USER=US10723947 @CGN 1.1 5315 @runat_23022006_085359_16224 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:**

1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	253	24.1	864	10 CL972569	CL972569 OsIFCC023
2	219	20.9	689	8 DN238319	DN238319 MUC4LH100
3	213	20.3	1305	4 CNS09200	XB811971 Arabidops
4	209	19.9	848	7 CV291360	CV291360 acof01-5ms
5	207	19.8	815	8 DR750621	DR750621 48-L02059
6	207	19.8	817	8 DN604709	DN604709 JCAT59576
7	207	19.8	829	5 BU636028	BU636028 044E12 In

8	207	19.8	1308	4	CNS09258	XB811501 Arabidops
9	207	19.8	1335	4	CNS091N5	XB832165 Arabidops
10	205	19.6	563	6	CB911506	CB911506 VVD132B12
11	205	19.6	596	6	CD007533	CD007533 VVB072E11
12	205	19.6	631	6	CD010195	CD010195 VVB104H08
13	205	19.6	650	6	CD010575	CD010575 VVB113D03
14	205	19.6	712	3	BM436387	BM436387 VVA003D01
15	204.5	19.5	546	10	CZ787328	CZ787328 OC_Ba015
16	204	19.5	548	2	BI074743	BI074743 IFI_15_F0
17	204	19.5	626	6	CD010039	CD010039 VVB103B05
18	203	19.4	761	9	CC728227	CC728227 OGCV57TM
19	203	19.4	780	8	DR930452	DR930452 EST112199
20	201	19.2	850	9	CC685007	CC685007 OGOAS10TV
21	201	19.2	907	9	CC685002	CC685002 OGOAS10TH
22	199	19.0	822	7	CK275343	CK275343 EST721421
23	199	19.0	851	7	CK274891	CK274891 EST720969
24	197	18.8	519	7	CV545348	CV545348 S81281.tx
25	197	18.8	582	1	AI488780	AI488780 EST247119
26	195.5	18.7	843	5	BO797187	BO797187 EST_6125
27	195	18.6	536	3	BM528344	BM528344 s8157C04
28	195	18.6	549	5	BU084004	BU084004 s8133903
29	195	18.6	577	3	BM271055	BM271055 s8104F11
30	195	18.6	579	3	BQ299156	BQ299156 s8104G08
31	195	18.6	587	5	BU081045	BU081045 s810G08
32	195	18.6	634	8	CX538017	CX538017 s13DNF54E
33	195	18.6	742	6	CA919328	CA919328 EST637046
34	195	18.6	780	7	CK248987	CK248987 EST732624
35	194.5	18.6	564	5	BQ588069	BQ588069 E012336-0
36	194.5	18.6	622	7	CV458983	CV458983 acof02-6ms
37	194.5	18.6	833	9	BZ734187	BZ734187 OGFPAQ22TC
38	194	18.5	678	6	CA800072	CA800072 s8177C07
39	194	18.5	723	7	CK255880	CK255880 EST739517
40	194	18.5	815	7	CK279398	CK279398 EST725476
41	194	18.5	820	7	CK245114	CK245114 EST728751
42	193.5	18.5	1021	10	CL012630	CL012630 ZMMBB053
43	192	18.3	640	10	CL925503	CL925503 OA_Aba003
44	192	18.3	661	6	CB003731	CB003731 VVB032E05
45	192	18.3	668	6	CB001303	CB001303 VVB005E07

ALIGNMENTS

RESULT 1

CL972569

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CL972569 864 bp DNA linear GSS 21-SEP-2004
OsIFCC023161 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.

CL972569.1 GI:52399671

GSS.

Oryza sativa (indica cultivar-group)

Oryza sativa (indica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 864)

Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,

Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,

Wong, G.K.S., Deng, X.W. and Wang, J.

An analysis of transcriptional regulation of the rice genome and

its comparison to Arabidopsis

Unpublished (2004)

Contact: Chen Chen

Department of Bioinformatic

Beijing Institute of Genomics

Chinese Academy of Sciences, Beijing 101300, China

Tel: 86-10-80481559

Fax: 86-10-80488676

Email: chenchen@genomics.org.cn

Rice genomic sequence.

Class: exon-trapped.

FEATURES Location/Qualifiers

1..864

source


```

LOCUS       CV291360               848 bp    mRNA    linear    EST 09-JUN-2005.
DEFINITION   aof01-5msl-b04 Aof01 Asparagus officinalis cDNA clone
aof01-5msl-b04 5', mRNA sequence.
ACCESSION    CV291360
VERSION      CV291360.1 GI:52577578
KEYWORDS     EST.
SOURCE       Asparagus officinalis (garden asparagus)
ORGANISM     Asparagus officinalis
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta, Liliopsida; Asparagales;
              Asparagaceae; Asparagus.
REFERENCE    1 (bases 1 to 848)
AUTHORS      dePamphilis,C., Carlson,J., Ma,H., Soltis,D., Soltis,P.,
              Oppenheimer,D., Frohlich,M., Doyle,J., Tanksley,S., Webb,M.,
              Leebens-Mack,J., Landherr,L., Flut,D. and Wall,K.
              Generation of ESTs from early male inflorescences of Asparagus
              officinalis
              Unpublished (2004)
COMMENT      Contact: Claude dePamphilis or James Leebens-Mack
              Mueller Laboratory
              Penn State University
              208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
              State University, University Park, PA 16802, USA
              Tel: 814 863 6413
              Fax: 814 865 9131
              Email: cwd3@psu.edu or jhl10@psu.edu
              The sequence provided is trimmed of vector and low quality regions.
              Full sequence and original trace file are available from the Plant
              Genome Network website (http://pgn.cornell.edu)
              Plate: aof01-5msl row: b column: 04
              Seq primer: M13F.
              Location/Qualifiers
                1..848
                  /organism="Asparagus officinalis"
                  /mol_type="mRNA"
                  /db_xref="PGN:aof01-5msl-b04"
                  /db_xref="taxon:4686"
                  /clone="aof01-5msl-b04"
                  /tissue_type="male inflorescences"
                  /lab_host="SOLR"
                  /clone_lib="Aof01"
                  /notes="Vector: pBluescript SK (+/-); Site 1: EcoRI;
                  Site 2: XhoI; this is a directionally cloned,
                  non-normalized library. This library has been generated by
                  the Floral Genome Project (FGP). The Floral Genome Project
                  is funded by NSF's Plant Genome Research Program
                  (DBI-0115684). More information about the project can be
                  obtained at http://fgp.bio.psu.edu"

ALIGNMENT SCORES:
Pred. No.:      5,48e-10      Length:      848
Score:          209.00      Matches:     65
Percent Similarity: 40.9%      Conservative: 23
Best Local Similarity: 30.2%      Mismatches: 81
Query Match:    19.9%      Indels:     46
DB:             7           Gaps:       6

US-10-723-947-77 (1-187) x CV291360 (1-848)
Qy      6 GlyLeuCysGlyAlaAsnAenCysProArGLeuMetValSerProLeHisHisHis 25
Db      2 GGCAAACTCAACGAATGTTGCTCTACTGTATCGCGCTCAACCGCGCGTAGCG 61
Qy      26 HisHisHisGlnCluHisGlnLeuCysGluTyrGlnPheAlaHisGlyAsnHisHis 45
Db      62 GGCCACGACGGCGCTCAAGCGCTGCGAGGAGTTCCTCAATCTTTCCAAAGGACACGTTG 121
Qy      46 HisHisHisGlySerAlaAlaAspTyrProValProProProAspAsnPheAsp 65
Db      122 GCGTGGCTGTTTAACTACTCAAGCGCGCGCGCGGCGGCAACAGGCGCTGAGGAGTC--- 178
Qy      66 HisArgArgThrTrpThrArgProPheHisGluThrAlaAlaGly----- 81

```

```

Db      179 -----GCTAGGCCCATGCAAGCTCGCGCGCGCGGGGTTTAAATTATTT 223
Qy      82 -----AenSerSerArgLeuThrLeuGluValGlyAlaGlyGly 94
Db      224 GAGGGATTGAGGGGTTCTTGTAAACCGGGGAGGTGACCTTGATGTTGTTGACGGG 283
Qy      95 -----GlnHisMetAlaHisLeuValGlnProProAla 105
Db      284 ACGAGCTCGCGGACTCGATGTCAGGCAGTCGCGCTCTGTGGATGTTCTTCGCGCGG 343
Qy      106 ArgAlaHis-----lLeuValProPheTyrGlyAlaPheThrAsn 119
Db      344 ATGGGGCATGTTGGATCGCGTGGTAACTGTCATGCTTCTTCGCGC----- 388
Qy      120 ThrIleSerAsnGluAlaIleMetThrIleAsp-----ThrGlu 132
Db      389 -----GTTGGCCCGCTACGTTTACCTCGACCCCTCGGCAACNACTGCCACAGCC 442
Qy      133 MetMetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaValMetArg 152
Db      443 GAAGGCACGACCGCGAGCAAGCGCAACCGCAACCGCAGAGAGCAAAAGTGTGAGG 502
Qy      153 TyrArgGluLeuArgLeuArgArgTyrArgPheGlnIleArgTyrGluSerArgGly 172
Db      503 TACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 562
Qy      173 AlaTyrAlaGluLeuArgProArgValAsnGlyArgPheVallys 187
Db      563 GCGTATGCGAGATGAGCGCGGAGGATAAAGGCGGATTTGCGAG 607

RESULT 5
DR750621/c
LOCUS       DR750621               815 bp    mRNA    linear    EST 19-JUL-2005
DEFINITION   48-L020593-065-004-H06-SELB MP1Z-ADIS-065d Arabidopsis thaliana
              cDNA clone 004-H06, mRNA sequence.
ACCESSION    DR750621
VERSION      DR750621.1 GI:71035961
KEYWORDS     EST.
SOURCE       Arabidopsis thaliana (thale cress)
ORGANISM     Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
              rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE    1 (bases 1 to 815)
AUTHORS      Paz-Ares,J., Valencia,A., Costantino,P., Vittorioso,P., Davies,B.,
              Gilmartin,P., Giraudat,J., Parcy,F., Reindl,A., Sablowski,R.,
              Coupland,G., Martin,C., Angenent,G.C., Baumelein,H., Mock,H.P.,
              Carbonero,P., Colombo,L., Tonelli,C., Engstrom,P.,
              Droege-Laser,W., Gatz,C., Kavanagh,T., Kushnir,S., Zabeau,M.,
              Laux,T., Hordsworth,M., Ruberti,I., Ratcliff,F., Smeekens,S.,
              Somsich,I., Weishaar,B. and Traas,J.
              REGIA, an EU project on functional genomics of transcription
              factors from Arabidopsis thaliana
              Comp. Funct. Genomics 3 (2), 102-108 (2002)
              Contact:
              Paz-Ares, Costantino, Vittorioso, Davies, Gilmartin, Giraudat, Parcy, Sablowski,
              Coupland, Martin, Angenent, Baumelein, Carbonero, Colombo, Tonelli,
              Engstrom, Droege-Laser, Gatz, Kavanagh, Kuehnir, Zabeau, Laux, Hordsworth,
              Ruberti, Smeekens, Somsich, Weishaar, Traas
              Bielefeld University, Institute for Genome Research
              Universitaetstrasse 25, D-33594 Bielefeld, Germany
              Email: bernd.weishaar@uni-bielefeld.de
              AGI: A75G57660; SeqAnalysis: full CDS correct; Translation: full
              good
              Data analysis performed in the frame of REGULATORS (Exploiting
              inter-species conservation in promoter sequences to identify
              regulators of reproductive development and physiological
              performance), a Trilateral Co-Operation in Plant Genomics between
              Spain (MCYT), France (GENOPLANTE) and Germany (GABI) coordinated by
              G. Coupland (coupland-ad-mpiz-koeln.mpg.de). Authors: Vincent
              Thureau (thp-orsay UMR8618 CNRS-UPS, thureau-ad-ibp.u-psud.fr) and
              Alain Lecharny (URGV-Evry UMR INRA-CNRS-UEVE,

```


Alignment Scores:		Location/Qualifiers	
Pred. No.:	8.19e-10	1..829	
Score:	207.00	/organism="Arabidopsis thaliana"	
Percent Similarity:	47.4%	/mol_type="mRNA"	
Best Local Similarity:	32.2%	/ecotype="Columbia"	
Query Match:	19.8%	/db_xref="taxon:3702"	
DB:	8	/dev_stage="Plant 3 weeks old, three days post infection"	
		/clone_lib="Infected Arabidopsis Leaf"	
		/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dT selected."	
US-10-723-947-77 (1-187) x DN604709 (1-817)			
QY	32	GlnLeuCysGluTyrGlnPhePheAlaHisGlyAsnHisHisHisHisHisGlySer	51
DB	526	CGGCTTATTGATTTCGAGTTCCGAATTCGTTCAATCATCAAAACACGCCGAGGA	467
QY	52	AlaAlaAspTyrProVal	66
DB	466	GATAGTCTTGTTCGGTTTCAGAGAAACAGAGCCTCTCCGTTAACTAATCATGATCAT	407
QY	67	-----ArgArgThrTrpThrArgProPheHisGlu	76
DB	406	TGCTTCGATATTGATTTCGAGATCAAAAGCTCTCTGCTTTCACCTTACCTTCAATCA	347
QY	77	ThrAlaAlaAlaGlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlnHis	96
DB	346	GTACGCCACAGTGTTCGACTTCT-----TCTATTGAATACGGT	308
QY	97	MetAlaHisLeuValGlnProProAlaArgAlaHisIleValProPheTyrGlyGlyAla	116
DB	307	-----GTAGTTCTCT-----GACGGAAC	290
QY	117	PheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetValGly	136
DB	289	ACAAACAACCTCTGTTAAACCGGACGACGATC-----ACTAGCTCGACGACTGCT	242
QY	137	ProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLys	156
DB	241	GGTGATCATCAACGAGCTCTTATGATAGAGAGCTAGGTTTTCAGGTACAGAGAGAAG	182
QY	157	ArgLysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGlu	176
DB	181	AGAAAGACAGGAATTTGAGAGAGAGATTCGTACCTTCGAGGAACCTTATCGCAGAG	122
QY	177	LeuArgProArgValAsnGlyArgPheValLys	187
DB	121	TCACGCCCAAGGATCAAAAGCGGTTTGCAGAA	89
RESULT 7			
BU636028			
LOCUS			
DEFINITION			
044812 Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA			
sequence.			
*ACCESSION			
BU636028			
VERSION			
BU636028.1 GI:23303283			
KEYWORDS			
Arabidopsis thaliana (thale cress)			
ORGANISM			
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;			
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;			
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
1 (bases 1 to 829)			
Lundsgaard M., Emmersen, J., Nielsen, K.L., Wilson, I., Somerville, S.			
and Welinder, K.G.			
EST sequencing of Erysiphe cichoracearum infected Arabidopsis			
plants			
Unpublished (2002)			
Contact: Karen G. Welinder			
Institut for bioteknologi			
Aalborg Universitet			
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark			
Tel: +45 96358467			
Fax: +45 98141808			
Email: kgw@bio.au.dk.			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
CNS09ZSB			
LOCUS			
DEFINITION			
Arabidopsis thaliana Full-length cDNA Complete sequence from clone			
GSLTPGH12811 of Hormone Treated Callus of strain col-0 of			
Arabidopsis thaliana (thale cress).			
ACCESSION			
BX831501			
VERSION			
BX831501.1 GI:42456535			
KEYWORDS			
HTC; GSLT cDNA.			
SOURCE			
Arabidopsis thaliana (thale cress)			
ORGANISM			
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;			

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1308)
AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.

TITLE Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1308)
GENOSCOPE.

AUTHORS Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

COMMENT The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES Location/Qualifiers

1..1308

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="GSLTPGH12H11"

/issue_type="Hormone Treated Callus"

/ecotype="Col-0"

/plasmid="pCMVSPORT_6"

1..1308

/gene="At5g57660"

ORIGIN

Alignment Scores:

Pred. No.: 1..51e-09 Length: 1308

Score: 207.00 Matches: 55

Percent Similarity: 47.4% Conservative: 26

Best Local Similarity: 32.2% Mismatches: 50

Query Match: 19.8% Indels: 40

DB: 4 Gaps: 6

US-10-723-947-77 (1-187) x CNS092SB (1-1308)

QY 32 GlnLeuCysGlyThrGlnPhePheAlaHisGlyAsnHisHisHisHisHisGlySer 51

DB 579 CGCGTTATTGATTTCGAGTTTCGGAATTCGTTCAATCATCATCAAAACACCGCGAGGA 638

QY 52 AlaAlaAspTyrProVal-----ProProProProAspAsnPheAspHis 66

DB 639 GATAGTCTTTGTTCCGGTTCAGACGAAACAGAGSCCTCTCCCGTTAACTAACATGATCAT 698

QY 67 -----ArgArgThrTropThrArgProPheHisGlu 76

DB 699 TCGTTCGATTGATTTCGAGATCAAGCTCTGCTTTTACTTACCTTCTCTCAATCA 758

QY 77 ThrAlaAlaGlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHis 96

DB 759 GTCAGCCACAGTGTTCGACTTCT-----TCPTATTGAATACGTT----- 797

QY 97 MetAlaHisLeuValGlnProProAlaArgAlaHisIleValProPheTyrGlyGlyAla 116

DB 798 -----GTAGTTCTCT-----GACGGAAAC 815

QY 117 PheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGly 136

Db 816 ACAACAACTCTGTCTAAACCGGAGCAGATC-----ACTAGTCGACGACTGGT 863

QY 137 ProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLys 156

Db 864 GGTGATCATCATACGAGCTCTTATGATGAGAGCTAGGTTTGTAGGTACAGAGAGAAG 923

QY 157 AsgLYsAsgArgTyrAspLYsGlnIleAsgTyrGluSerArgLYsAlaTyrAlaGlu 176

Db 924 AGAAGAACACGGAATTTGAGAAGAGGATTCGTTCGTTCCGAGGAAGCTTATGCAGAG 983

QY 177 LeuArgProArgValAsnGlyArgPheValLys 187

Db 984 TCACGCCCAAGCATCAAGGCGGTTTGCGAAA 1016

RESULT 9

CNS09YN5 1335 bp mRNA linear HTC 06-FEB-2004

LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone

DEFINITION GSLTPGH562A01 of Hormone Treated Callus of strain col-0 of

Arabidopsis thaliana (thale cress).

ACCESSION EX832165

VERSION EX832165.1 GI:42455085

KEYWORDS HTC; GSLT cDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1335)

AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,

Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,

Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.

Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome

Annotation

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1335)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

COMMENT The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out

full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.

URGV INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis

genome released by MIPS (Munich Information center for Protein

Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full

length

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES Location/Qualifiers

1..1335

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/db_xref="taxon:3702"

/clone="GSLTPGH562A01"

/issue_type="Hormone Treated Callus"

/ecotype="Col-0"

/plasmid="pCMVSPORT_6"

1..1335

/gene="At5g57660"

ORIGIN

Alignment Scores:

Pred. No.: 1.55e-09 Length: 1335

Score: 207.00 Matches: 55

Percent Similarity: 47.4% Conservative: 26

```
Best Local Similarity: 32.2% Mismatches: 50
Query Match: 19.8% Indels: 40
DB: 4 Gaps: 6

US-10-723-947-77 (1-187) x CNS09YN5 (1-1335)

QY 32 GlnLeuCysGluTyrGlnPhePheAlaHisGlyAsnHisHisHisHisHisGlySer 51
DB 584 CGGCTATTGATTCGAGTTTCGGAATTCGTTCAATCATCATCAAAACACGCCGAGGA 643
QY 52 AlaAlaaspTyrProVal-----ProProProProAspAsnPheAspHis 66
DB 644 GATAGTCTGTTCGGTTCAGACGAAACAGAGCCCTCTCCGTTACTACTAATGATCAT 703
QY 67 -----ArgArgThrTrrPrrArgProPheHisGlu 76
DB 704 TGCTTCGATATTGATTTCTGCAGATCAAAAGCTCTCTGCTTTCTACCTTCTCAATCA 763
QY 77 ThrAlaAlaAlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlnHis 96
DB 764 GTCAGCCACAGTGTTCGACTTCT-----TCTATTGAATACGGT----- 802
QY 97 MetAlaHisLeuValGlnProProAlaArgAlaHisIleValProPheTyrGlyGlyAla 116
DB 803 -----GTAGTTCT-----GACGGAAAC 820
QY 117 PheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetValGly 136
DB 821 ACAACAACACTCTGTTAAACCGGACGACGATC-----ACTAGCTCGACGACTGT 868
QY 137 ProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLys 156
DB 869 GGTGATCATCAAGCGAGCTCTATGAGTACAGAGCTAGGTTTTCGAGTACAGAGAGA 928
QY 157 ArgLysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGlu 176
DB 929 AGAAGAAGACAGGAATTTGAGAGAGCATTCGTTCGCTTCGAGGAAGCTTATGCAGAG 988
QY 177 LeuArgProArgValAsnGluArgPheValLys 187
DB 989 TCACGGCCAAAGATCAAGACCGGCTTTCGAAA 1021

RESULT 10
CB911506 563 bp mRNA linear EST 25-APR-2003
LOCUS VVD132B12 372903 An expressed sequence tag database for abiotic
DEFINITION stressed berries of Vitis vinifera var. Chardonnay Vitis vinifera
CDNA clone VVD132B12 5, mRNA sequence.
CB911506
ACCESSION CB911506.1 GI:30126167
VERSION CB911506.1
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
Cushman, J.C.
1 (bases 1 to 563)
An expressed sequence tag database for abiotic stressed berries of
Vitis vinifera var. Chardonnay
Unpublished (2002).
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 132 row: B column: 12
Seq primer: T3 20mer

High quality sequence stop: 563.
Location/Qualifiers
1. 563
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVD132B12"
/tissue_type="berries"
/dev_stages="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone_lib="An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site_1:
EcoRI; Site_2: XhoI"

FEATURES
source
1. 563
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVD132B12"
/tissue_type="berries"
/dev_stages="mixed; 8, 9, 11, 13, 15, 16 weeks daf"
/clone_lib="An expressed sequence tag database for abiotic
stressed berries of Vitis vinifera var. Chardonnay"
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site_1:
EcoRI; Site_2: XhoI"

ORIGIN
Alignment Scores:
Pred. No.: 7,91e-10 Length: 563
Score: 205.00 Matches: 54
Percent Similarity: 46.3% Conservative: 21
Best Local Similarity: 33.3% Mismatches: 53
Query Match: 19.6% Indels: 34
DB: 6 Gaps: 5

US-10-723-947-77 (1-187) x CB911506 (1-563)
QY 44 HisHisHisHisHisHisGlySerAlaAlaAsp-----Tyr 55
DB 60 CACCATCATCACCACCACTGCGGTGGAAATGATGTAGTTCGCGTTCAAGCCAAAGAT 119
QY 56 ProValProPro-----ProProAspAsn-----PheAspHisArgArg 68
DB 120 CCTCACCTCCGGTCACGAACCACTGCTGCAATTTGTTGAACTGGATTTCTCTCGA 179
QY 69 ThrTrrPrrArgProPheHisGluThrAlaAlaAlaGlyAsnSerSerArgLeuThrLeu 88
DB 180 TCAAGAGCTCTGCTGTACATATACAGCTCAATCTTAAAGCCAAAGCATTCATCTTCA 239
QY 89 GluValGlyAla-----GlyGlyGlnHisMetAlaHisLeuValGlnProProAla 105
DB 240 GATGTTGGGTTGTCCAGATGGGAACCTCACTCTGATACATCATCTACCTACCTCG 299
QY 106 ArgAlaHisIleValProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAla 125
DB 300 ATGAAGCAAGTAGCGGAGCGCGCGCGGCTTCTACTGGGAGTCAACGCGACCAATTA 359
QY 126 IleMetThrIleAspThrGluMetValGlyProAlaHisTyrProThrMetGlnGlu 145
DB 360 -----TCTGGAATGGAT 371
QY 146 ArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgArgTyrAspLysGln 165
DB 372 CCGAAGCGAGGGTGTTCGAGGTACAGAGAGAGAGAAAGAACCGGAAATTCGAGAAACC 431
QY 166 IleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArgPhe 185
DB 432 ATCATAGTGGCTCCAGAAAGAGCTTACCGCGAGAGCGCGTCCAGAAATCAAGAGCGCTTC 491
QY 186 ValLys 187
DB 492 GCAGAG 497

RESULT 11
CB007533 596 bp mRNA linear EST 02-MAY-2003
LOCUS VVB072E11 334194 An expressed sequence tag database for abiotic
DEFINITION stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera
CDNA clone VVB072E11 5, mRNA sequence.
CB007533
ACCESSION CB007533.1 GI:30324271
VERSION CB007533.1
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; Vitaceae; Vitis.
1 (bases 1 to 596)
Cramer, G.R. and Cushman, J.C.
An expressed sequence tag database for abiotic stressed leaves of
Vitis vinifera var. Chardonnay
Unpublished (2002)
JOURNAL
COMMENT
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 0 row: E column: 11
Seq primer: T3 20mer
High quality sequence stop: 596.
Location/Qualifiers
source
1. 596
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVB072E11"
/tissue_type="leaf"
/dev_stage="juvenile and adult"
/clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/notes="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN
Alignment Scores:
Pred. No.: 8 52e-10 Length: 596
Score: 205.00 Matches: 54
Percent Similarity: 46.3% Conservative: 21
Best Local Similarity: 33.3% Mismatches: 53
Query Match: 19.6% Indels: 34
DB: 6 Gaps: 5

US-10-723-947-77 (1-187) x CD007533 (1-596)

QY 44 HisHisHisHisHisHisGlySerAlaAlaAasp-----Tyr 55
Db 121 CACCATCATCACCACCACCTGCGGTGGAATGATGGTTCGGTTCAGGCAAGAT 180
QY 56 ProValProPro-----ProProAspAsn-----PheAspHisArgArg 68
Db 181 CCCTCACCCTCGGTCAACCAACCAACCTGCTGACAAATGTTTGAACCTGGATTTCTCTCGA 240
QY 69 ThrTrpThrArgProPheHisGluThrAlaAlaAlaGlyAsnSerSerArgLeuThrLeu 88
Db 241 TCAAAGCTCTCTCCCTACCATATACAGCTCAATCTCTAAGCCAAAGCATTCCTCTCA 300
QY 89 GluValGlyAla-----GlyGlyGlnHisMetAlaHisLeuValGlnProProAla 105
Db 301 GATGTTGGGGTGTCTCCAGATGGGAAGTCACTCCATGCTGATACATCTTACCTTCG 360
QY 106 ArgAlaHisIleValProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAla 125
Db 361 ATCAAGCAAGTACAGCGCGCGCGCGGTCTACTGGAGTCAAGCGACCAATTA 420
QY 126 IleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThrMetGlnGlu 145
Db 421 -----TCTGGAATGGAT 432
QY 146 ArgAlaAlaLysValMetArgTyrArgGlyLysArgGlyArgArgTyrAspLysGln 165
Db 433 CGCGAAGCGGGTGTGTAGGTACAGAGAGAGAGAGAACCGGAAATTCGAGAAACC 492

QY 166 IleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArgPhe 185
Db 493 ATCAGATACGCTCCAGAAAGCCTACGCGACGCTCCAGAAATCAGAGCCGCTTC 552
QY 186 ValLys 187
Db 553 GCAAG 558
RESULT 12
CD010195 631 bp mRNA linear EST 02-MAY-2003
LOCUS VVB104H08 341909 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera CDNA clone VVB104H08 5, mRNA sequence.
DEFINITION
ACCESSION CD010195 GI:30326933
VERSION CD010195.1
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
REFERENCE 1 (bases 1 to 631)
AUTHORS Cramer G.R. and Cushman, J.C.
TITLE An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay
JOURNAL Unpublished (2002)
COMMENT Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
PCR Primers
FORWARD: T3 20mer
BACKWARD: T7 21mer (backward)
Plate: 1 row: H column: 08
Seq primer: T3 20mer
High quality sequence stop: 631.
Location/Qualifiers
source
1. 631
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVB104H08"
/tissue_type="leaf"
/dev_stage="juvenile and adult"
/clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/notes="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN
Alignment Scores:
Pred. No.: 9 18e-10 Length: 631
Score: 205.00 Matches: 54
Percent Similarity: 46.3% Conservative: 21
Best Local Similarity: 33.3% Mismatches: 53
Query Match: 19.6% Indels: 34
DB: 6 Gaps: 5

US-10-723-947-77 (1-187) x CD010195 (1-631)

QY 44 HisHisHisHisHisHisGlySerAlaAlaAasp-----Tyr 55
Db 121 CACCATCATCACCACCACCTGCGGTGGAATGATGGTTCGGTTCAGGCAAGAT 180
QY 56 ProValProPro-----ProProAspAsn-----PheAspHisArgArg 68

Db 181 CCTCACTCCGCTCAGAACACCCTGCTGACAATGTTTGAAGTGGATTCTCTCGA 240
 Qy 69 ThrTrpThrArgProPheHisGluThrAlaAlaGlyAsnSerSerArgLeuThrLeu 88
 Db 241 TCAAGCTCTCTGCTTACACTATACAGCTCATCTCTAAGCCAAAGCATTTCTCTTCA 300
 Qy 89 GluValGlyAla-----GlyGlyGlnHisMetAlaHisLeuValGlnProProAla 105
 Db 301 GATGTTGGGGTGTCCAGATGGAACTGCAACTCCATGCTGATACATCTCTACCTCTCG 360
 Qy 106 ArgAlaHisIleValProPheThrGlyGlyAlaPheThrAsnThrIleSerAsnGluAla 125
 Db 361 ATGAAGCAAGTACGCGGCGCGGGTCTACTGGGAGTCAAGCGACCCCAATTA 420
 Qy 126 IleMetThrIleAspThrGluMetValGlyProAlaHisIleValGlnProProAla 105
 Db 421 -----TCTGGAATGGAT 432
 Qy 146 ArgAlaAlaValMetArgTyArgGlyGlnHisMetAlaHisLeuValGlnProProAla 165
 Db 433 CGCGAAGCGAGGTGTGAGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
 Qy 166 IleArgTyGluSerArgLysAlaTyAlaGluLeuArgProArgValAsnGlyArgPhe 185
 Db 493 ATCAGATACGCTCCAGAAAGCCTACGCGAGAGCGCTCAAGAAATCAAGAGCGCGTTTC 552
 Qy 186 Vallys 187
 Db 553 GCAAG 558
 RESULT 13
 CD010575
 LOCUS
 DEFINITION
 CD010575 650 bp mRNA linear EST 02-MAY-2003
 VVB113D03 342669 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera CDNA clone VVB113D03 5, mRNA sequence.
 CD010575
 EST.
 SOURCE
 Vitis vinifera
 Vitis vinifera
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
 1 (bases 1 to 650)
 Cramer,G.R. and Cushman,J.C.
 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay
 Unpublished (2002)
 Contact: Cushman JC
 Department of Biochemistry
 University of Nevada
 MS200, Reno, NV 89557-0014, USA
 Tel: 775-784-1918
 Fax: 775-784-1650
 Email: jcushman@unr.edu
 PCR Primers
 FORWARD: T3 20mer
 BACKWARD: T7 21mer (backward)
 Plate: 1 row: D column: 03
 Seq primer: T3 20mer
 High quality sequence stop: 650.
 Location/Qualifiers
 1. 650
 /organism="Vitis vinifera"
 /mol_type="mRNA"
 /db_xref="taxon:29760"
 /clone="VVB113D03"
 /tissue_type="leaf"
 /dev_stage="juvenile and adult"
 /clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
 /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site_1: source

Alignment Scores:
 Pred. No.: 9,548-10 Length: 650
 Score: 205.00 Matches: 54
 Percent Similarity: 46.3% Conservative: 21
 Best Local Similarity: 33.3% Mismatches: 53
 Query Match: 19.6% Indels: 34
 DB: 6 Gaps: 5
 US-10-723-947-77 (1-187) x CD010575 (1-650)
 Qy 44 HisHisHisHisHisHisGlySerAlaAlaAap-----Tyr 55
 Db 121 CACCATCATCACCACTGCGGTGAATGATGTAGTTCGCGTTCAAGCCAAAGAT 180
 Qy 56 ProValProPro-----ProProAspAsn-----PheAspHisArgArg 68
 Db 181 CCTCACTCCGCTCAGAACACCCTGCTGACAATGTTTGAAGTGGATTCTCTCTCGA 240
 Qy 69 ThrTrpThrArgProPheHisGluThrAlaAlaGlyAsnSerSerArgLeuThrLeu 88
 Db 241 TCAAGCTCTCTGCTTACACTATACAGCTCATCTCTAAGCCAAAGCATTTCTCTTCA 300
 Qy 89 GluValGlyAla-----GlyGlyGlnHisMetAlaHisLeuValGlnProProAla 105
 Db 301 GATGTTGGGGTGTCCAGATGGAACTGCAACTCCATGCTGATACATCTCTACCTCTCG 360
 Qy 106 ArgAlaHisIleValProPheThrGlyGlyAlaPheThrAsnThrIleSerAsnGluAla 125
 Db 361 ATGAAGCAAGTACGCGGCGCGGGTCTACTGGGAGTCAAGCGACCCCAATTA 420
 Qy 126 IleMetThrIleAspThrGluMetValGlyProAlaHisIleValGlnProProAla 145
 Db 421 -----TCTGGAATGGAT 432
 Qy 146 ArgAlaAlaValMetArgTyArgGlyGlnHisMetAlaHisLeuValGlnProProAla 165
 Db 433 CGCGAAGCGAGGTGTGAGGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492
 Qy 166 IleArgTyGluSerArgLysAlaTyAlaGluLeuArgProArgValAsnGlyArgPhe 185
 Db 493 ATCAGATACGCTCCAGAAAGCCTACGCGAGAGCGCTCAAGAAATCAAGAGCGCGTTTC 552
 Qy 186 Vallys 187
 Db 553 GCAAG 558
 RESULT 14
 BM436387
 LOCUS
 DEFINITION
 BM436387 712 bp mRNA linear EST 31-JAN-2002
 VVA003D01 52357 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera CDNA clone VVA003D01 5, mRNA sequence.
 BM436387
 EST.
 SOURCE
 Vitis vinifera
 Vitis vinifera
 ORGANISM
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; Vitaceae; Vitis.
 1 (bases 1 to 712)
 Cramer,G.R. and Cushman,J.C.
 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay
 Unpublished (2002)
 Contact: Cushman JC
 Department of Biochemistry
 University of Nevada

BcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UnizapXR vector and cDNA synthesis kit."

MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu

PCR Primers

FORWARD: T3 20mer
BACKWARD: T7 21mer

Plate: 003 row: D column: 01

Seq primer: T3 20mer

High quality sequence stop: 712.

Location/Qualifiers

FEATURES

source

1..712
/organism="Vitis vinifera"
/mol_type="mRNA"
/db_xref="taxon:29760"
/clone="VVA003D01"
/tissue_type="leaf"
/dev_stage="juvenile and adult"
/clone_lib="An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay"
/notes="Vector: Lambda Uni-Zap XR, Bluescript SK-, Site 1: EcoRI; Site 2: XhoI; Library construction was performed according to Stratagene's recommended protocol for the Lambda UniZapXR vector and cDNA synthesis kit."

ORIGIN

Alignment Scores:
Pred. No.: 1,07e-09 Length: 712
Score: 205.00 Matches: 54
Percent Similarity: 46.3% Conservative: 21
Best Local Similarity: 33.3% Mismatches: 53
Query Match: 19.6% Indels: 34
DB: 3 Gaps: 5

US-10-723-947-77 (1-187) x BM436387 (1-712)

Qy 44 HisHisHisHisHisHisGlySerAlaAlaAAsp-----Tyr 55
Db 232 CACCATCATCACCACCACCTCGCGGTGGAATGTTGTTAGTTCGCGTTCAAGCCAAAGAT 291
Qy 56 ProValProPro-----ProProAspAsn-----PheAspHisArgArg 68
Db 292 CCTCATCTCCGTCACGAACCAACCCTGCTGCAATGTTTGAACCTGGATTTCTCTCGA 351
Qy 69 ThrTrpThrArgProPheHisGluThrAlaAlaAlaGlyAsnSerSerArgLeuThrleu 88
Db 352 TCAAAGCTCTGCTTACAACTATACAGCTCAATCTCTAAGCCAAAGCAATTTTCATCTTCA 411
Qy 89 GluValGlyAla-----GlyGlyGlnHisMetAlaHisLeuValGlnProProAla 105
Db 412 GATGTTGGGGTGTCCCAATGGGAACCTGCACTCCATGCTGTGATACATCTTACCTTCG 471
Qy 106 ArgAlaHisIleValProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAla 125
Db 472 ATGAACCAAGTGAGCGGCGCGCGGGTCTTACTGGGAGTCAAGCCCAATTA 531
Qy 126 IleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThrMetGlnGlu 145
Db 532 -----TCTGGAATGGAT 543
Qy 146 ArgAlaAlaLysValMetArgTyrArgGluLysArgArgArgTyrAspLysGln 165
Db 544 CCGGAAGCGAGGTGTGAGGTACAGAGAGAGAGAGAACCGGAATTCAGAAAC 603
Qy 166 IleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArgPhe 185
Db 604 ATCAGATACGCTCCAGAAAGGCTACGCCGAGACCGCTCCAAAGATCAAGCGCGCTTC 663
Qy 186 ValLys 187
Db 664 GCAAAG 669
RESULT 15

CZ787328/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1..546

/organism="Oryza coarctata"

/mol_type="genomic DNA"

/db_xref="taxon:77588"

/clone="OC_Ba0151B03"

/tissue_type="leaves"

/dev_stage="mature"

/lab_host="DH10B"

/clone_lib="OC_Ba"

/note="Vector: pGIBAC1; Site 1: HindIII; Site 2: HindIII"

ORIGIN

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

US-10-723-947-77 (1-187) x CZ787328 (1-546)

Qy 91 GlyAlaGlyGlyGlnHisMetAlaHisLeuValGlnProAlaArgAlaHisIle-Va 110

Db 392 GGGGCGGCGCGC-----GTCCGGTCCACCTTCAT 363

Qy 110 lProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAs 130

Db 362 GCCATTCTCGGGAGCAGACACTTGAAGGCACCTTG---AACGATAGCACAGAGGTTGG 306

Qy 130 pThrGluMetMetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysVa 150

Db 305 GGAAGGCATGACGGCGCGCGCGAGGT-----GACCTGGCAATTCGAGAGGAAAGCCAAAGAT 252

Qy 150 lMetArgTyrArgGluLysArgLysArgArgTyrAspLysGlnIleArgTyrGluSe 170

Db 251 CATGAGGTACAAAG 192

Qy 170 rArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArgPheValLys 187

Db 191 GAGGAGGCGCTATCTGAGATGAGGCGCAAGGTTAAAGGGCGGCTTCGCAAG 140

CZ787328 546 bp DNA linear GSS 26-JUL-2005
OC_Ba0151B03.f OC_Ba Oryza coarctata genomic clone OC_Ba0151B03
5', genomic survey sequence.

CZ787328

CZ787328.1 GI:71227181

GSS.

Oryza coarctata (Porteresia coarctata)

Oryza coarctata

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 546)

Kim H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,

Rao, X., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and

Wing, R.

OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute

Unpublished (2005)

Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: TAA TAC GAC TCA CTA TAG GG

BACKWARD: CAC TCA TTA GGC ACC CCA

Plate: 0151 row: B column: 03

Seq primer: TAA TAC GAC TCA CTA TAG GG

Class: BAC ends.

Location/Qualifiers

1..546

/organism="Oryza coarctata"

/mol_type="genomic DNA"

/db_xref="taxon:77588"

/clone="OC_Ba0151B03"

/tissue_type="leaves"

/dev_stage="mature"

/lab_host="DH10B"

/clone_lib="OC_Ba"

/note="Vector: pGIBAC1; Site 1: HindIII; Site 2: HindIII"

Search completed: February 23, 2006, 11:40:49
Job time : 3670 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2006, 10:37:57 ; Search time 490 Seconds

(without alignments)
2543.464 Million cell updates/sec

Title: US-10-723-947-77

Perfect score: 1048

Sequence: 1 MSMSCLCGANNCPRLWSP.....YESRKAYAEIPLRVNGRFVK 187

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 496997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+pn.model -DEV=xl
-Q=/abs/ABSWEB/spool/US10723947/runat_23022006_085355_16167/app_query.fasta.1
-DB=N Geneseq -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abs03p
-USER=US10723947 @CGN_1_1096 @runat_23022006_085355_16167 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSBBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 21.*

1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
7: Geneseqn2002bs.*
8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
1	1035	98.8	996	13	ADS19577	ADS19577	One grain
2	907.5	86.6	975	13	ADS19581	ADS19581	Langdon (
3	816	77.9	7051	13	ADS19576	ADS19576	One grain
4	768.5	73.3	639	13	ADS19590	ADS19590	Winter ba

ALIGNMENTS

RESULT 1
ADS19577
ID ADS19577 standard; cDNA; 996 BP.
AC ADS19577;
XX ADS19577;
DT 30-DEC-2004 (first entry)
DE One grained wheat DV92 ZCCT1 cDNA.
KW One grained wheat; chromosome 5a; ss; APTALAL1; API; vernalisation;
KW flowering; ZCCT1; ZCCT2; vrn1; vrn2; CARG box; plant; gene.
XX Triticum monococcum.
XX US2004205848-A1.
XX 14-OCT-2004.
XX 26-NOV-2003; 2003US-00723947.
XX 11-APR-2003; 2003US-00412137.
XX (REGC) UNIV CALIFORNIA.
XX Dubcovsky J, Yan L, Loukoianov A;
XX WPI; 2004-728059/71.

5 756 72.1 642 13 ADS19593
6 730.5 69.7 639 13 ADS19584
7 729.5 69.6 639 13 ADS19587
8 670.5 64.0 2913 13 ADS19580
9 590 56.3 1985 13 ADS19589
10 572.5 54.6 2043 13 ADS19592
11 547.5 52.2 5734 13 ADS19583
12 538 51.3 3454 13 ADS19586
13 258 24.6 1078 13 ADS16783
14 255 24.3 1078 13 ADS16786
15 254 24.2 1078 13 ADS16780
16 207 19.8 1068 12 ADN72948
17 207 19.8 1297 6 ABN98249
18 207 19.8 1370 13 ADX31777
19 207 19.8 1374 3 AAC46126
20 207 19.8 1377 3 AAC32326
21 207 19.8 1404 13 ADX30238
22 199.5 19.0 1703 14 ADM16416
23 198.5 18.9 1122 13 ADV09279
24 194 18.5 1388 14 AEB65256
25 193.5 18.5 1728 14 ADM16414
26 189.5 18.1 1385 13 ADS16785
27 188.5 18.0 2723 13 ADS16782
28 188.5 18.0 2723 13 ADS16782
29 188 17.9 1101 2 AAT29510
30 187.5 17.9 2723 13 ADS16779
31 185.5 17.7 577 12 ADJ33390
32 184.5 17.6 1441 13 ADT20147
33 183 17.5 1406 14 ADM16807
34 180.5 17.2 1101 2 AAT29509
35 180 17.2 698 13 ADX31789
36 180 17.2 971 3 AAC51945
37 180 17.2 1125 3 AAC46448
38 180 17.2 1202 13 ADX45392
39 180 17.2 1553 13 ADX13438
40 180 17.2 1593 13 ADT14899
41 179 17.1 939 4 AAC90637
42 176.5 16.8 596 13 ACN60093
43 176.5 16.8 885 6 ABZ12460
44 176.5 16.8 1002 12 ADJ39403
45 176.5 16.8 1075 13 ADX47666

ADS19593 Winter ba
ADS19584 One grain
ADS19587 Langdon ()
ADS19580 Langdon ()
ADS19589 Winter ba
ADS19592 Winter ba
ADS19583 One grain
ADS19586 Langdon ()
ADS16783 Lhd4-rela
ADS16786 Lhd4-rela
ADS16780 Lhd4-rela
ADN72948 Thale cre
ABN98249 Arabidops
ADX31777 Plant ful
AAC46126 Arabidops
AAC32326 Arabidops
ADX30238 Plant ful
ADM16416 E Grandis
ADV09279 B. pendul
AEB65256 Rice geno
ADM16414 E Grandis
ADS16499 Plant ful
ADS16782 Lhd4-rela
ADM16782 Lhd4-rela
AAT29510 CONSTANS
ADJ31789 Plant ful
AAC51945 Arabidops
AAC46448 Arabidops
ADX45392 Plant ful
ADX13438 Plant ful
ADT14899 Plant cDN
AAC90637 Strawberry
ACN60093 Cotton gy
ABZ12460 Arabidops
ADJ39403 Plant cDN
ADX47666 Plant ful

DR P-PSDB; ADS19578.
XX. New recombinant ZCCT1 protein coding sequence useful for altering a
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.
XX
XX
PS Claim 1; SEQ ID NO 75; 115pp; English.
XX
CC The invention relates to a recombinant ZCCT1 protein (2n finger and CCT
CC domain protein) coding sequence comprising a nucleic acid that hybridizes
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
CC the identification of to genes, vrn1 identified as AP1 (APETALA1) and
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
CC have been localised to chromosome 5a of one grained wheat, Triticum
CC monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a
CC binding site for ZCCT1 termed the CARG box. Also included are a vector
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell
CC comprising the vector, a transgenic plant comprising the recombinant
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits
CC ZCCT1 repression of AP1), a seed from the transgenic plant, a method for
CC altering a plant's response to vernalisation and a molecular marker for
CC vrn2 derived from ADS19577. The genetic construct is an interference RNA
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
CC a repression defective ZCCT1 protein operably linked to a promoter or a
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
CC operably linked to a promoter. The present sequence is a plant ZCCT1 cDNA
CC sequence.
XX
SQ Sequence 996 BP; 281 A; 273 C; 224 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 7.23e-86 Length: 996
Score: 1035.00 Matches: 185
Percent Similarity: 99.5% Conservative: 1
Best Local Similarity: 98.9% Mismatches: 1
Query Match: 98.8% Indels: 0
DB: 13 Gaps: 0

US-10-723-947-77 (1-187) x ADS19577 (1-996)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 109 ATGTTCATGTCATGCGGTTGTGCGCGCCCAACACTGCCGCGCTCATGTCCTCGCCC 168

QY 21 IleHisHisHisHisHisGlnGlnHisGlnLeuCysGluTyrGlnPhePheAla 40
DB 169 ATTACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 228

QY 41 HisGlyAsnHisHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro 60
DB 229 CATGGCAACCAACCACCACCACCACCACCACCACCACCACCACCAGTACCCAGTCCACCGCG 288

QY 61 ProAspAsnPhaAspHisArgThrTrpThrArgProPheHisGluThrAlaAlaAla 80
DB 289 CCAGACAACTTCGACCACCGAGAACATGGACACAGACCACTTTTCATGAACACAGCAGCGCA 348

QY 81 GlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHisLeu 100
DB 349 GGGAAACAGCAGCAGGCTTCAGTGGAGGTGGCGCGCAGCGCGCCCAACACATGGCTCACCTTA 408

QY 101 ValGlnProProAlaArgAlaHisIleValProPheTyrGlyGlyAlaPheThrAsnThr 120
DB 409 GTGCGACCAACCGGACAGCCACATCGTGCATTTACGGAGGTGCATTCACCAACT 468

QY 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyr 140
DB 469 ATTAGCAATGAAGCAATCATGACTATTTCACAGAGATGATGTCGGGCTGCCCATATT 528

QY 141 ProThrMetGlnGluArgAlaAlaValMetArgTyrArgGluHisArgLysArgArg 160
DB 529 CCCCAATCAGGAGAGACGACGGAAGGTGATGAGGTATAGGAGGAAGGAGGCGG 588

QY 161 ArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180
DB 589 CGCTATGACAAAGCAATCCGATACGAGTCCAGAAAGCTTACGCTGAGCTTCGGCCATGG 648

QY 181 ValHengGlyArgPheValLys 187
DB 649 GTCACACGGCCGCTTTGTCAAG 669

RESULT 2
ADS19581
ID ADS19581 standard; cDNA; 975 BP.
XX
AC ADS19581;
XX
DT 30-DEC-2004 (first entry)
XX
DE Langdon (tetraploid) wheat ZCCT1 cDNA.
XX
KW Wild emmer wheat; sg; APETALA1; AP1; vernalisation; flowering; ZCCT1;
XX ZCCT2; vrn1; vrn2; CARG box; plant; gene.
OS Triticum turgidum; subsp. dicoccoides.
XX
PN US2004205848-A1.
XX
PD 14-OCT-2004.
XX
PF 26-NOV-2003; 2003US-00723947.
XX
PR 11-APR-2003; 2003US-00412137.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Dubcovsky J, Yan L, Loukoianov A;
XX
DR WPI; 2004-728059/71.
DR P-PSDB; ADS19582.
XX
PT New recombinant ZCCT1 protein coding sequence useful for altering a
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.
XX
PS Disclosure; SEQ ID NO 79; 115pp; English.
XX
CC The invention relates to a recombinant ZCCT1 protein (2n finger and CCT
CC domain protein) coding sequence comprising a nucleic acid that hybridizes
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
CC the identification of to genes, vrn1 identified as AP1 (APETALA1) and
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
CC have been localised to chromosome 5a of one grained wheat, Triticum
CC monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a
CC binding site for ZCCT1 termed the CARG box. Also included are a vector
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell
CC comprising the vector, a transgenic plant comprising the recombinant
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits
CC ZCCT1 repression of AP1), a seed from the transgenic plant, a method for
CC altering a plant's response to vernalisation and a molecular marker for
CC vrn2 derived from ADS19577. The genetic construct is an interference RNA
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
CC a repression defective ZCCT1 protein operably linked to a promoter or a
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
CC operably linked to a promoter. The present sequence is a plant ZCCT1 cDNA
CC sequence.
XX
SQ Sequence 975 BP; 276 A; 263 C; 218 G; 218 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.91e-74 Length: 975
Score: 907.50 Matches: 168
Percent Similarity: 91.4% Conservative: 3

Db 3421 TGAATACACCACTACAAAAAGTAGCACCATCTAACCATTTCATATATTTCTCACATAA 3480
QY 109 ----- 109
Db 3481 TTCCTGTTAAATTAGCTGCTCGATTGTTCTCCTGAAAAAGATATACGGGATGATCTGG 3540
QY 109 ----- 109
Db 3541 ATATTCTTTAAATTTCTATGGAGGCATAGAGTTGTGTTTGTATTAGTTAGTCAGAAAT 3600
QY 109 ----- 109
Db 3601 TGTATGGGTTGTCAAAATCATCATCTACATATATATCTTATTTCCTTTTTCCTTTTGGACCAAC 3660
QY 109 ----- 109
Db 3661 AGAAGGTAATCAGTCATATCATCTGACTGCTGAAAATTAGACTTGTGTGCAATACTAATACTA 3720
QY 109 ----- 109
Db 3721 ACCAACTCGACCGGCACAGCTGGGGGAAGACTTTAATCAAGCTGTAGCTAGAGCTTAAT 3780
QY 109 ----- 109
Db 3781 AATATAACATATCTTTATGGATCAAGCAATACATATGCGCTCAATTTCTCAACTTGTG 3840
QY 109 ----- 109
Db 3841 AATATCTATCTGGAGTCCACACTTTATGTTAATTAATGACAAAGTTTGTGNAATGGAC 3900
QY 109 ----- 109
Db 3901 AATATACATACTGGATCGATGCACCCTTTTCTCAATTTATGTTGCTCAATTAATTAATGATT 3960
QY 109 ----- 109
Db 3961 GTTATTTAGTATTTCAATTTATCTTGAGCTAGTCTTTTGGCAAGTCTGTAGCTCATATATAA 4020
QY 109 ----- 109
Db 4021 CTGATACTACTCCACGATAGCTTGGTAGTGGCGGGTGATCGATCTACCGAGTTTAT 4080
QY 109 ----- 109
Db 4081 AAAAAGTATGATCGGCTGCAAAAAAGAAACAAACCCATACAAAAATGGAAGAGATCC 4140
QY 109 ----- 109
Db 4141 TTGTTTAGTTAGTTTGCATCAGAAAAATGCTTAATTAGTTACTGTGCTATCAATCTTTTGA 4200
QY 109 ----- 109
Db 4201 ACATGCGATGTTTACCCCAACGAGCCAGATCAATATTATGATGAAGTTAGCGCTTTT 4260
QY 109 ----- 109
Db 4261 AAAAAGTATGATGATATACATGATACAGGGCTACACATGTACATATAACCTTA 4320
QY 109 ----- 109
Db 4321 ATTAAAAAGTATATTTGTAGACCAATTTGATTTTGGACGGTGGCGATCTTTTGGAAAAA 4380
QY 109 ----- 109
Db 4381 TGGCAGAGGTTGTAGTCTTCCATGCTCCAGAAATAGATGTTACATCAATCAAGTGCATC 4440
QY 109 ----- 109
Db 4441 TCTGTAATGAAATGGATCATTTTCTAGTTAATTAGAGACCAATTAGATCTTCTATAACA 4500
QY 109 ----- 109
Db 4501 GGGAGATATCAAGTACGTATCTGCTACCCATAAGAAAGTACATACTGCGATCTTATGAT 4560

QY 110 -----ValProPheTyrGlyValaPheThrAsnThrIleSer 122
Db 4561 TATTTTCTCTTGTGATGTTCCAGGTGCCATTTACGGAGGTGCATTTACCAACACTATTAGC 4620
QY 123 AAGGluAlaIleMetThrIleAspThrGluMetMetValGlyProIleHisTyrProThr 142
Db 4621 AATGAAGCAATCATGACTATTGACACAGAGATGATGGTGGGCGCTGCCCATTTATCCACA 4680
QY 143 MetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgArgArgTyr 162
Db 4681 ATGCAAGAGAGAGAGAGAGAGTGTAGGTATAGGAGAGAGAGAGAGAGAGAGAGAGAG 4740
QY 163 AspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsn 182
Db 4741 GACAAAGCAATCCGATACGATCCAGAAAGCTTACGCTGAGCTTCGGCCATGGGTCAAC 4800
QY 183 GlyArgPheValLys 187
Db 4801 GGCCGCTTTGTCAAG 4815

RESULT 4

ADSI9590
ID ADSI9590 standard; cDNA; 639 BP.

AC ADSI9590;

DT 30-DEC-2004 (first entry)

XX Winter barley ZCCT-Ha cDNA.

DE Barley; ss; APETALAI; APl; vernalisation; flowering; ZCCT1; ZCCT2; vrn1;

KW vrn2; CarG box; plant; gene.

XX Hordeum vulgare.

XX US2004205848-A1.

XX 14-OCT-2004.

XX 26-NOV-2003; 2003US-00723947.

XX 11-APR-2003; 2003US-00412137.

XX (REG) UNIV CALIFORNIA.

XX Dubcovsky J, Yan L, Loukoianov A;

XX WPI; 2004-728059/71.

DR P-PSDB; ADSI9591.

PT New recombinant ZCCT1 protein coding sequence useful for altering a
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.

PS Disclosure; SEQ ID NO 88; 115bp; English.

XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
XX domain protein) coding sequence comprising a nucleic acid that hybridizes
XX to the barley ZCCT1 cDNA appearing as ADSI9577. The patent also discloses
XX the identification of to genes, vrn1 identified as APl (APETALAI) and
XX vrn2 identified as ZCCT1 controlling vernalisation of flowering in
XX temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
XX have been localised to chromosome 5a of one grained wheat, Triticum
XX monococcum. ZCCT1 is the repressor of APl whose promoter contains a
XX binding site for ZCCT1 termed the CarG box. Also included are a vector
XX comprising the recombinant ZCCT1 protein coding sequence above, a call
XX comprising the vector, a transgenic plant comprising the recombinant
XX ZCCT1 protein coding sequence above (or a genetic construct that inhibits
XX ZCCT1 repression of APl), a seed from the transgenic plant, a method for
XX altering a plant's response to vernalisation and a molecular marker for
XX vrn2 derived from ADSI9577. The genetic construct is an interference RNA
XX construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense

CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
CC a repression defective ZCCT1 protein operably linked to a promoter or a
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
CC operably linked to a promoter. The present sequence is a plant ZCCT cDNA
CC sequence.

XX
SQ Sequence 639 BP; 164 A; 208 C; 159 G; 108 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,48e-61 Length: 639
Score: 768.50 Matches: 148
Percent Similarity: 82.6% Conservativity: 9
Best Local Similarity: 77.9% Mismatches: 28
Query Match: 73.3% Indels: 5
DB: 13 Gaps: 3

US-10-723-947-77 (1-187) x ADS19593 (1-639)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 1 ATGTCCATGTCATGTGGTTGTGGCGCGCAGCAACTGGCGGTACCAATGATGTGCGCC 60
QY 21 IleHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPhePheAla 40
DB 61 GTTCTTCTTCATCATCACCATCATCAGCAACACCCACTGCACGAGTACCACTTCTTCGCC 120
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyr---ProValProPro 59
DB 121 CAAGGT-----CACCACACCAACCAACAGCGCGGCGGAGTACCAACCCACCGCCCA 174
QY 60 ProProAspAsnPheAspHisArgArgTrrTrrArgProPheHisGluThrAlaAla 79
DB 175 CGCCAGACAAATGCCACCAACACATCATGTGACCAACCGCGTTTCATGAACAGCAGCT 234
QY 80 AlaGlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHis 99
DB 235 CCAGAGAACAGCAGCAGGCTCACACGGGAGGTGGACGCGCGGCGGCAACACATGGCTCAC 294
QY 100 LeuValGlnProProAla-----ArgAlaHisIleValProPheTyrGlyGlyAlaPhe 117
DB 295 CTGCTCGACGCCACCGCGCGCGCGCAAGAGCCACCATCGTGCCTTCCTGCAGAGTGCATT 354
QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
DB 355 GCCAGCACTATTAGCAACGCAACGATCATGACTATTGATACAGAAATGATGGGGCCT 414
QY 138 AlaHisTyrProThrMetGlnGluAlaAlaLysValMetArgTyrArgGluLysArg 157
DB 415 GCCTATAATCCACGATGCAGGAGAGAGAGCGGCAAGGTGATGAGGTACAGGGAGAGAGG 474
QY 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
DB 475 AGAGCGCGCGCTTATGACAAAGCAAAATCCGCTACGAGTCCAGAAAGCTTACCGCGGAGCTC 534
QY 178 ArgProArgValAsnGlyArgPheValLys 187
DB 535 AGGCCACGGGTCAATGGCGCGCTTGGCAG 564

RESULT 5

ADS19593
ID ADS19593 standard; cDNA; 642 BP.

XX
AC ADS19593;

XX
DT 30-DEC-2004 (first entry)

XX
DE winter barley ZCCT-Hb cDNA.

KW Barley; ss; APETAL1; AP1; vernalisation; flowering; ZCCT1; ZCCT2; vrn1;
KW vrn2; CARG box; plant; gene.

XX
OS Hordeum vulgare.

PN US2004205848-A1.

XX
PD 14-OCT-2004.

XX
PF 26-NOV-2003; 2003US-00723947.

XX
PR 11-APR-2003; 2003US-00412137.

XX
PA (REGC) UNIV CALIFORNIA.

XX
PI Dubcovsky J, Yan L, Loukoianov A;

XX
WPI; 2004-728059/71.

XX
P-PsDB; ADS19594.

PT New recombinant ZCCT1 protein coding sequence useful for altering a
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.

XX
PS Disclosure; SEQ ID NO 91; 115pp; English.

XX
CC The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
CC domain protein) coding sequence comprising a nucleic acid that hybridises
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
CC the identification of to genes, vrn1 identified as AP1 (APETAL1) and
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
CC have been localised to chromosome 5a of one grained wheat, Triticum
CC monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a
CC binding site for ZCCT1 termed the CARG box. Also included are a vector
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell
CC comprising the vector, a transgenic plant comprising the recombinant
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits
CC ZCCT1 repression of AP1), a seed from the transgenic plant, a method for
CC altering a plant's response to vernalisation and a molecular marker for
CC vrn2 derived from ADS19577. The genetic construct is an interference RNA
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
CC a repression defective ZCCT1 protein operably linked to a promoter or a
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
CC operably linked to a promoter. The present sequence is a plant ZCCT cDNA
CC sequence.

XX
SQ Sequence 642 BP; 165 A; 206 C; 163 G; 108 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2,11e-60 Length: 642
Score: 756.00 Matches: 146
Percent Similarity: 82.6% Conservativity: 11
Best Local Similarity: 76.8% Mismatches: 29
Query Match: 72.1% Indels: 4
DB: 13 Gaps: 3

US-10-723-947-77 (1-187) x ADS19593 (1-642)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
DB 1 ATGTCCATGTCATGCGTTGTGGCGCGCAGCAATGCGCGTATCAGATGATGCGCC 60
QY 21 IleHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPhePheAla 40
DB 61 GTTCTTCTTCATCATCACCATCATCAGGAACATCGCGAGCGGAGTACCACTTCTTCGCC 120
QY 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyr---Pro 59
DB 121 CAAGGT---CACCACCAACCAACAGCGCGGCGGAGTACCAACCGCCACAGCCA 177
QY 60 ProProAspAsnPheAspHisArgArgTrrTrrArgProPheHisGluThrAlaAla 79
DB 178 CGCGCGCGCAATGGCACCACCGCAGATCATGGCCACGCTGTTTCATGAACAGCAGCT 237
QY 80 AlaGlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHis 99

Db 238 CCAGTGATAGACACAGGCTCACAAGAGGTGGACGCGAGCGGCCAACAGATGGCTCAC 297
Qy 100 LeuValGlnProProLa-----ArgAlaHisIleValProPheTyrGlyAlaPhe 117
|||:|||||
Db 298 CTGCTGACGACCGCGCGCGCCCAAGAGCCACCATGTCCTTCGCGGGAGTGCAATTC 357
Qy 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetValGlyPro 137
|||:|||||
Db 358 ACCAACACATATTAGCAACGCAACGATCATGCTATTGATACAGAGATGATGGCGGGACT 417
Qy 138 AlaHisTyrProThrMetGlnGluArgAlaAlaIleValMetArgTyrArgGluLysArg 157
|||:|||||
Db 418 GCTATAGTCCACAGTATGACGAGGAAGAGCAAGGTGATGAGGTACAGGAGAGAGG 477
Qy 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
|||:|||||
Db 478 AGAAGCGCGGCTATGACAAAGCAATCCGTACGAGTCCAGAAAGCTTACCGCGAGCTT 537
Qy 178 ArgProArgValAsnGlyArgPheValLys 187
Db 538 AGGCCACGGGTCAACGGCGCTTTGTCAAG 567
RESULT 6
ADSI19584
ID ADS19584 standard; cDNA; 639 BP.
XX
AC ADS19584;
XX
DT 30-DEC-2004 (first entry)
XX
DE One grained wheat DV92 ZCCT2 cDNA.
XX
KW One grained wheat; chromosome 5a; ss; APETALAI; AP1; vernalisation;
flowering; ZCCT1; ZCCT2; vrn1; vrn2; CARG box; plant; gene.
XX
OS Triticum monococcum.
XX
PN US2004205848-A1.
XX
PD 14-OCT-2004.
XX
PP 26-NOV-2003; 2003US-00723947.
XX
PR 11-APR-2003; 2003US-00412137.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Dubcovsky J, Yan L, Loukoianov A;
XX
DR WPI; 2004-728059/71.
DR P-PSDB; ADS19585.
XX
PT New recombinant ZCCT1 protein coding sequence useful for altering a
plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.
XX
PS Disclosure; SEQ ID NO 82; 115pp; English.
XX
CC The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
domain protein) coding sequence comprising a nucleic acid that hybridises
to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
the identification of to genes, vrn1 identified as AP1 (APETALAI) and
vrn2 identified as ZCCT1 controlling vernalisation of flowering in
temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
have been localised to chromosome 5a of one grained wheat, Triticum
monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a
binding site for ZCCT1 termed the CARG box. Also included are a vector
comprising the recombinant ZCCT1 protein coding sequence above, a cell
comprising the vector, a transgenic plant comprising the recombinant
ZCCT1 protein coding sequence above (or a genetic construct that inhibits
ZCCT1 repression of AP1), a seed from the transgenic plant, a method for
altering a plant's response to vernalisation and a molecular marker for
vrn2 derived from ADS19577. The genetic construct is an interference RNA

CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
CC a repression defective ZCCT1 protein operably linked to a promoter or a
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
CC operably linked to a promoter. The present sequence is a plant ZCCT cDNA
CC sequence.
XX
SQ Sequence 639 BP; 162 A; 197 C; 171 G; 109 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4,69e-58 Length: 639
Score: 730.50 Matches: 144
Percent Similarity: 81.8% Conservative: 11
Best Local Similarity: 75.8% Mismatches: 28
Query Match: 69.7% Indels: 7
DB: 13 Gaps: 4

US-10-723-947-77 (1-187) x ADS19584 (1-639)

Qy 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
Db 1 ATGTCCATGTATCGGGTTTGTGGCGCAAGCAGCTCCCGCCACCATGATGATCTCGGCC 60
Qy 21 IleHisHisHisHisHisHisHisGlnLeuCysGluTyrGlnPheAla 40
Db 61 GTT-----CTTCAGCATCAGGAACACACAGCTGGCTGGCGGATACAGTCTTCACC 111
Qy 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60
Db 112 CAAGGC---CACCACCACCACCACCAGCGCGCGGGCGGACTACCCACCGCCACCGCCA 168
Qy 61 ProAsp---AsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79
Db 169 CCGTCGGGCAATTGCCACCACTGCAGATCATGGACCAACACCGCTTTTCATGAACACAGCAGT 228
Qy 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
Db 229 GCAGGAAACAGCAGCAGACTCAGCTGGAGGTAGATGACGCGCGGCAAAACATGCTCAC 288
Qy 100 LeuValGlnProProAlaAlaAlaHis-----IleValProPheTyrGlyAlaPhe 117
Db 289 CTGCTGACGACCCCGGACGCGCCCAAGACCACTCGTGCCATCTTGGGGGCTGCATTC 348
Qy 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
Db 349 ACCAGCACTATTAGCAATGCAACATCATGACTATTGATACAGAGATGATGTTGGGGCT 408
Qy 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157
Db 409 GCCCAATAATCTGACGATCGAGAGAGAGAGGAGGTGATGAGGTACAGGAGAGAGG 468
Qy 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
Db 469 AAGAGCGGTGCTATGACAGCAATCCGCTACGAGTCCAGAAAGCTTACCGCGAGCTC 528
Qy 178 ArgProArgValAsnGlyArgPheValLys 187
Db 529 AGGCCACGGGTCAATGGCTGCTTTGTCAAG 558

RESULT 7

ADSI19587

ID ADS19587 standard; cDNA; 639 BP.

XX

AC ADS19587;

XX

DT 30-DEC-2004 (first entry)

XX

DE Langdon (tetraploid) wheat ZCCT2 cDNA.

XX

KW Wild emmer wheat; ss; APETALAI; AP1; vernalisation; flowering; ZCCT1;

XX

KW ZCCT2; vrn1; vrn2; CARG box; plant; gene.

XX

OS Triticum turgidum; subsp. dicoccoides.

XX US2004205848-A1.
 XX
 XX
 XX PD 14-OCT-2004.
 XX
 XX PF 26-NOV-2003; 2003US-00723947.
 XX
 XX PR 11-APR-2003; 2003US-00412137.
 XX
 XX PA (REGC) UNIV CALIFORNIA.
 XX
 XX PI Dubcovsky J, Yan L, Loukoianov A;
 XX
 XX DR WPI; 2004-728059/71.
 XX
 XX DR P-PSDB; ADS19588.
 XX
 XX PT New recombinant ZCCT1 protein coding sequence useful for altering a
 XX
 XX PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
 XX
 XX PT vernalization or flowering times.
 XX
 XX PS Disclosure; SEQ ID NO 85; 115pp; English.
 XX
 XX CC The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
 CC domain protein) coding sequence comprising a nucleic acid that hybridises
 CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
 CC the identification of to genes, vrn1 identified as AP1 (APETALA1) and
 CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in
 CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
 CC have been localised to chromosome 5a of one grained wheat, Triticum
 CC monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a
 CC binding site for ZCCT1 termed the CARG box. Also included are a vector
 CC comprising the recombinant ZCCT1 protein coding sequence above, a cell
 CC comprising the vector, a transgenic plant comprising the recombinant
 CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits
 CC ZCCT1 repression of AP1), a seed from the transgenic plant, a method for
 CC altering a plant's response to vernalisation and a molecular marker for
 CC vrn2 derived from ADS19577. The genetic construct is an interference RNA
 CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense
 CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
 CC a repression defective ZCCT1 protein operably linked to a promoter or a
 CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
 CC operably linked to a promoter. The present sequence is a plant ZCCT1 cDNA
 CC sequence.
 XX
 XX SQ Sequence 639 BP; 161 A; 200 C; 172 G; 106 T; 0 U; 0 Other;
 XX

Alignment Scores:
 Pred. No.: 639
 Score: 729.50 Matches: 143
 Percent Similarity: 81.6% Conservative: 12
 Best Local Similarity: 75.3% Mismatches: 28
 Query Match: 69.6% Indels: 7
 DB: 13 Gaps: 4

US-10-723-947-77 (1-187) x ADS19587 (1-639)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
 DB 1 ATGCCCATGTCATGCGGTTGTGCGCGCAAGCGACTGCCCGCACCACCATGATCTCGCCC 60
 QY 21 ILeHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
 DB 61 GTT-----CTTCAGCATCAGGAACAACACCGGCTCGCGAGTACCAGTCTTCACC 111
 QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 60
 DB 112 CAAGGC--CACACACACACACACACACGCGCGCGGAGTACCACCGCCACCGCCA 168
 QY 61 ProAsp---AsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79
 DB 169 CCGTCAGGCAATTGCCACCACTGCATGATGACACACCGGTTTCATGAACAGCAGCT 228
 QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99

XX DB 229 GCAGGGACAGCAGCAGGCTCAAGCTGGAGGTAGACGCGCGCCAAACATGGCTCAC 288
 XX
 XX QY 100 LeuValGlnProProAlaArgAlaHis-----IleValProPheTyrfGlyGlyAlaPhe 117
 XX
 XX DB 289 CTGCTGCAGCCACCGGCGCGCCCAAGAACCCACCATCGTGCCATTCTGCGGGGCTGCATTTC 348
 XX
 XX QY 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
 XX
 XX DB 349 ACCAGCATTATTAGCAATGCAACGATCATGATATTGATACAGAGATGATGTGGGGGCT 408
 XX
 XX QY 138 AlaHisTyfProThrMetGlnGluArgAlaIleValMetArgTyfArgGluLysArg 157
 XX
 XX DB 409 GCCATAATCTGACGATGCGAGGAGAGAGAGGCGAAGGTGATGAGGTACAGGAGAGAGG 468
 XX
 XX QY 158 LysArgArgArgTyfAspLysGlnIleArgTyfGluSerArgLysAlaTyfAlaGluLeu 177
 XX
 XX DB 469 AAGAGCGGCTGTATGACAAGCAAAATCCGCTATGATGATCCAGAAAGCTTACGCCGAGCTC 528
 XX
 XX QY 178 ArgProArgValAsnGlyValArgPheValLys 187
 XX
 XX DB 529 AGGCCACGCGTCATGCGCGCTTTGTCAAG 558
 XX

RESULT 8
 ADS19580
 ID ADS19580 standard; DNA; 2913 BP.
 XX
 XX AC ADS19580;
 XX
 XX DT 30-DEC-2004 (first entry)
 XX
 XX DE Langdon (tetraploid) wheat ZCCT1 genomic DNA.
 XX
 XX KW Wild emmer wheat; ds; APETALA1; AP1; vernalisation; flowering; ZCCT1;
 XX
 XX OS ZCCT2; vrn1; vrn2; CARG box; plant; gene.
 XX
 XX OS Triticum turgidum; subsp. dicoccoides.
 XX
 XX PN US2004205848-A1.
 XX
 XX PD 14-OCT-2004.
 XX
 XX PF 26-NOV-2003; 2003US-00723947.
 XX
 XX PR 11-APR-2003; 2003US-00412137.
 XX
 XX PA (REGC) UNIV CALIFORNIA.
 XX
 XX PI Dubcovsky J, Yan L, Loukoianov A;
 XX
 XX DR WPI; 2004-728059/71.
 XX
 XX DR P-PSDB; ADS19582.
 XX
 XX PT New recombinant ZCCT1 protein coding sequence useful for altering a
 XX
 XX PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
 XX
 XX PT vernalization or flowering times.
 XX
 XX PS Disclosure; SEQ ID NO 78; 115pp; English.
 XX
 XX CC The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
 CC domain protein) coding sequence comprising a nucleic acid that hybridises
 CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
 CC the identification of to genes, vrn1 identified as AP1 (APETALA1) and
 CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in
 CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
 CC have been localised to chromosome 5a of one grained wheat, Triticum
 CC monococcum. ZCCT1 is the repressor of AP1 whose promoter contains a
 CC binding site for ZCCT1 termed the CARG box. Also included are a vector
 CC comprising the recombinant ZCCT1 protein coding sequence above, a cell
 CC comprising the vector, a transgenic plant comprising the recombinant
 CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits
 CC ZCCT1 repression of AP1), a seed from the transgenic plant, a method for
 CC altering a plant's response to vernalisation and a molecular marker for

Db 1470 TCATTGGACAAAGGCCCGGAAGTTGTTCTCTCCATTGTCTAATAAATAAGAACAGT 1529
Qy 109 ----- 109
Db 1530 TACAGTCAAGTCAACACTGAATGAAATGGATCAAGTTTGGTTAAACAGAGACCAACT 1589
Qy 109 ----- 109
Db 1590 TATACCTTCATAAACAAGGAATATCAAGTACATATCTGTACCCACAAGAAAGTACACT 1649
Qy 110 ----- 120
Db 1650 TATGACTATTCTTCTTCTGATGTCAGGTCCTTCTGAGAGTGTCATCCCGAGCACT 1709
Qy 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetValGlyProAlaHisTyr 140
Db 1710 ATTACCAAGCAACGATCATGACTATTGATACAGAAATGATGGTGGGCTGCTTATAAT 1769
Qy 141 ProThrMetGlnGluArgAlaAlaValMetArgTyrArgGluLysArgLysArg 160
Db 1770 CCAACGATGCAGGAGAGAGCGAAGGTGATGAGGTACAGGAGAGAGAGAGGCGG 1829
Qy 161 ArgTyrAspLysGluIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180
Db 1830 CCTATGACAAACAATCCGCTACGAGTCCAGAAAGCTTACGCCGAGCTCAGGCCACGG 1889
Qy 181 ValAsnGlyArgPheValLys 187
Db 1890 GTCAATGGCGCTTTGCCAAG 1910

RESULT 10

ADSI19592
ID ADS19592 standard; DNA; 2043 BP.

XX AC ADS19592;
XX 30-DEC-2004 (first entry)
XX Winter barley ZCCT-Hb genomic DNA.
DE Barley; ds; APETALAI; APl; vernalisation; flowering; ZCCT1; ZCCT2; vrn1;
KW vrn2; CARG box; plant; gene.
XX Hordeum vulgare.
OS US2004205848-A1.
XX PD 14-OCT-2004.
XX 26-NOV-2003; 2003US-00723947.
XX 11-APR-2003; 2003US-00412137.
XX (REGC) UNIV CALIFORNIA.
XX Dubcovsky J, Yan L, Loukoianov A;
XX WPI; 2004-728059/71.
XX P-PSDB; ADS19594.
XX New recombinant ZCCT1 protein coding sequence useful for altering a
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.
XX Disclosure; SEQ ID NO 90; 115pp; English.
XX The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
CC domain protein) coding sequence comprising a nucleic acid that hybridises
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
CC the identification of to genes, vrn1 identified as APl (APETALAI) and
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
CC have been localised to chromosome 5a of one grained wheat, Triticum

CC monococcum. ZCCT1 is the repressor of APl whose promoter contains a
CC binding site for ZCCT1 termed the CARG box. Also included are a vector
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell
CC comprising the vector, a transgenic plant comprising the recombinant
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits
CC ZCCT1 repression of APl), a seed from the transgenic plant, a method for
CC altering a plant's response to vernalisation and a molecular marker for
CC vrn2 derived from ADS19577. The genetic construct is an interference RNA
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
CC a repressor defective ZCCT1 protein operably linked to a promoter or a
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
CC operably linked to a promoter. The present sequence is a plant ZCCT
CC genomic DNA sequence.

SQ Sequence 2043 BP; 567 A; 495 C; 413 G; 527 T; 0 U; 41 Other;

Alignment Scores:

Pred. No.: 6.95e-43 Length: 2043
Score: 572.50 Matches: 146
Percent Similarity: 30.3% Conservative: 11
Best Local Similarity: 28.2% Mismatches: 29
Query Match: 54.6% Indels: 332
DB: 13 Gaps: 4

US-10-723-947-77 (1-187) x ADS19592 (1-2043)

Qy 1 MetSerMetSerCysGlyLeuCysGlyValAlaAsnAsnCysProArgLeuMetValSerPro 20
Db 420 ATGTCCATGGCATGGGTTTGTGGCGGCCAGCAATTGCCCGTATCATGATGTGCGCC 479
Qy 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
Db 480 GTTCTCTTTCATCATCACCATCATCAGGAACATCGCAGCGCGAGTACAGTCTTCTGCC 539
Qy 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 59
Db 540 CAAGGT---CACCAACACCCACCCAGCGCGCGAGCAGACTACCCACCCAGCA 596
Qy 60 ProProAspAsnPheAspHisArgThrTrpThrArgProPheHisGluThrAlaAla 79
Db 597 CCGCGGCCAATTCGCCACCCAGCAGATCATGGGCCAGCGCTTTCATGAAACAGCAGT 656
Qy 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlyHisMetAlaHis 99
Db 657 CCAGTGAATAGCACAGGCTCACAAAGAGGTGGACGAGCGCGCGCAACAGATGCTCAC 716
Qy 100 LeuValGlnProProAla-Arg----- 106
Db 717 CTGCTGAGCCACCGCGCGCGCGCCCAAGAGCCACCACCTCGTGAGTACTACTGCTTAATCGTTC 776
Qy 106 ----- 106
Db 777 CATCTCTCCGATCGATGTGACTCTCTTCTTAACAAAATACACTTCTTAATTTCCATC 836
Qy 106 ----- 106
Db 837 TCAAAAAAAGCTAGCGCCATGTGACAGCTCATATATCTGTACATACTCCGTTAATTT 896
Qy 106 ----- 106
Db 897 ATGCTGGTTCGATTGTAATTTTACCAGGAGAAAGTTTGTGTTGTATCAGTTGATGCAC 956
Qy 106 ----- 106
Db 957 AAGACTGGATGCTCAGATCATCAGTCACACATCATATATTTATTTTATTTATTTGAC 1016
Qy 106 ----- 106
Db 1017 TAACAAGTAATCAGTTAATTCCTTTTATGGGGTCAAGCAACATATGTCCAGCCTTCATG 1076
Qy 106 ----- 106

Db 1077 TTAATTCCTTGGCAGAGTTTGTGAATANAAGATATATATTGGATCAATGCACCTACC 1136
Qy 106 ----- 106
Db 1137 TCTTCTCATTTTATGTGNCATTTAAAAATTTGAATGCTATTTTGTATTAATTTCTC 1196
Qy 106 ----- 106
Db 1197 NTGAGCTAGTGTGGAAGCTTATAGCTCAATTTAACTGGAANNNNNNNNNNNNNNNN 1256
Qy 106 ----- 106
Db 1257 NNNNNNNCGAGTTTCATGAAGCTGATCAAGATCAGTNCAGAAAGGCCAAACCTCNCGA 1316
Qy 106 ----- 106
Db 1317 AATGGAATTNCGATCTCTGTTAANTAGTTTGGATCAGGAATNGGCTACTTAATTAATTG 1376
Qy 106 ----- 106
Db 1377 CTACCAATNTATGAAGATGGCATGTTCTCTCAAAATGATCCAGCTCACAATTTTGG 1436
Qy 106 ----- 106
Db 1437 TGAAGTTAAACATTTTGTAGCAATTCATAAAAGGTGCATAGATGTACAGGGCTACAGGTAC 1496
Qy 107 ----AlaHis----- 108
Db 1497 ACAGCGACATAATACCGCTAGTTAAACATATATGATGAGCAATTTGTTGGCAAT 1556
Qy 108 ----- 108
Db 1557 GCGCTTCTTGGACATAATGGCCGGGAAATGTTCTCTTCCATTTCTTAAACATAGA 1616
Qy 108 ----- 108
Db 1617 ACAGTTAGAATCAAGTGCACCACTGAATGAGATGGTCAATTTTGGTTAACGAGAGAC 1676
Qy 109 -----IleVal 110
Db 1677 CAACTATACGTTATAAACACTGTACTCTCACCATTGTTTCTCTCTCGATGTTCCAGT 1736
Qy 110 lProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAs 130
Db 1737 GCATTTCCCGGAGTGCATTTACCAACACTATTAGCAACGCAACGATCATGACTATTGA 1796
Qy 130 pThrGluMetMetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysVa 150
Db 1797 TACAGAGATGATGGCGGGGACTGCCTATAGTCCACAGATGCAGGAAGAGAAAGT 1856
Qy 150 lMetArgTyrArgGluLysArgLysArgArgTyrAspLysGlnIleArgTyrGluSe 170
Db 1857 GATGAGGTACAGGGAGAAGGAAGGCGGCTATGACAAAGCAATTCGCTACGAGTC 1916
Qy 170 rArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyArgPheValLys 187
Db 1917 CAGAAAGCTTACCGCGAGCTTAGGCCACGGGTCAACGGCGCTTTGTCAAG 1968

RESULT 11

ADSI9583
ID ADS19583 standard; DNA; 5734 BP.
XX
AC ADS19583;
XX
DT 30-DEC-2004 (first entry)
XX
DE One grained wheat DV92 ZCCT2 genomic DNA.
XX
KW One grained wheat; chromosome 5a; ds; APETAL1; API; vernalisation;
KW flowering; ZCCT1; ZCCT2; vrnl; vrn2; CARG box; plant; gene.
XX
OS Triticum monococcum.
XX

PN US2004205848-A1.
XX
PD 14-OCT-2004.
XX
PF 26-NOV-2003; 2003US-00723947.
XX
PR 11-APR-2003; 2003US-00412137.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Dubcovsky J, Yan L, Loukoianov A;
XX
DR WPI; 2004-728059/71.
DR P-PSDB; ADS19585.
XX
PT New recombinant ZCCT1 protein coding sequence useful for altering a
PT plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
PT vernalization or flowering times.
XX
PS Disclosure; SEQ ID NO 81; 115pp; English.
XX
CC The invention relates to a recombinant ZCCT1 protein (Zn finger and CCT
CC domain protein) coding sequence comprising a nucleic acid that hybridises
CC to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
CC the identification of to genes, vrnl identified as API (APETAL1) and
CC vrn2 identified as ZCCT1 controlling vernalisation of flowering in
CC temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
CC have been localised to chromosome 5a of one grained wheat, Triticum
CC monococcum. ZCCT1 is the repressor of API whose promoter contains a
CC binding site for ZCCT1 termed the CARG box. Also included are a vector
CC comprising the recombinant ZCCT1 protein coding sequence above, a cell
CC comprising the vector, a transgenic plant comprising the recombinant
CC ZCCT1 protein coding sequence above (or a genetic construct that inhibits
CC ZCCT1 repression of API), a seed from the transgenic plant, a method for
CC altering a plant's response to vernalisation and a molecular marker for
CC Vrnl derived from ADS19577. The genetic construct is an interference RNA
CC construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense
CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
CC a repression defective ZCCT1 protein operably linked to a promoter or a
CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
CC operably linked to a promoter. The present sequence is a plant ZCCT
CC genomic DNA sequence.
XX
SQ Sequence 5734 BP; 1563 A; 1278 C; 1220 G; 1673 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4,936-40 Length: 5734
Score: 547.50 Matches: 145
Percent Similarity: 28.2% Conservative: 11
Best Local Similarity: 26.2% Mismatches: 27
Query Match: 52.2% Indels: 371
DB: 13 Gaps: 5

US-10-723-947-77 (1-187) x ADS19583 (1-5734)
Qy 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAenCysProArgLeuMetValSerPro 20
Db 2589 ATGTCATGTCATGCGGTTTGTGCGCGCAAGCTGCGCCACCAATGATCTCGCC 2648
Qy 21 IleHisHisHisHisHisHisGlnGluHisGlnLeuCysGlyTyrGlnPheAla 40
Db 2649 GTT-----CTTCAGCATCAGGAACAACACTGGCTGGCGGAGTACCAGTCTTCACC 2699
Qy 41 HisGlyAsnHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro 60
Db 2700 CAAGGC---CACCACCAACCAACCAACCGCGCGGAGTACCACCGCCGCCCA 2756
Qy 61 ProAsp---AsnPheAspHisArgThrTTPThrArgProPheHisGluThrAlaAla 79
Db 2757 CGTCGCGCAATTTGCCACCACTGCAGATCATGACCAACCGCTTCATGAACAGCAGCT 2816
Qy 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHis 99

Db 2817 GCAGGAAACAGCAGCAGCTACGCTGGAGGTAGATGCAGGGCGCCAAACATGGCTCAC 2876
QY 100 LeuValGlnProAlaArg----- 106
|||:|||||
Db 2877 CTGCTGACGCCACCGCAGCCAGAACCAACCATCGTGAGTAGTACTACTGCTTAATTG 2936
QY 106 ----- 106
Db 2937 TTCCAGCTCTTGCCGATCGCTGGGGCTCCTTGTAACAAAAGTTCCCTTTTACGTAATCT 2996
QY 106 ----- 106
Db 2997 CCACTACTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCTCCCGCATCTCAAAAAAGT 3056
QY 107 ----- 109
|||
Db 3057 TAGCGCCATGTAACAGCTCATATATCTGTTCACATAATTCTGTTAATTATGCTGTGTCAA 3116
QY 109 ----- 109
Db 3117 TTATAATCTCCAAGGACGAAAGTTTGTGTTTGTATCATGTTGATGAACAAGAAATGGGAA 3176
QY 109 ----- 109
Db 3177 CTCACATCATCAGTTACACATACATACATCTTATTTTATTTGATCAACAAGGTAATCA 3236
QY 109 ----- 109
Db 3237 GTTAATTCCTTTATGGGAACAAGCAATACATATGTCACGCCCTTCATGTTAATTCCTTCA 3296
QY 109 ----- 109
Db 3297 CAAAGTTTGTGAATGGAACATATATATATCTGGATCAATGACCCCTCTTTCTCAITTTAT 3356
QY 109 ----- 109
Db 3357 GTGGTCAATTGAATTTTAGTGCTATTTATATATTTTAAATTTCTTAAAGCTGTTTG 3416
QY 109 ----- 109
Db 3417 TAAGCTTATAGCTCATGTATACAGATACACTCTCCCAATAATGCTTCGTAGTGCCGG 3476
QY 109 ----- 109
Db 3477 GTGATCAATCTACCGAGTTTCAAAAACATGATCGGATCAGATCCAAAACAGACCAAAACC 3536
QY 109 ----- 109
Db 3537 TCACGAAATAGAAACAAGATCCTTGTGTTAATAGTTTGCACGAGGAATGCTACTTAA 3596
QY 109 ----- 109
Db 3597 TTACTTTCTCATCTTATGAACATGGCATGTTTCTCACATATGTTGACCCAGATCACA 3656
QY 109 ----- 109
Db 3657 ATGTTGACGGAGTTAAACATTTTAGCAATTCATAAAACCATGCACAGATGTACAGGGC 3716
QY 109 ----- 109
Db 3717 TAGCGTATGCACATACATAATACACCTAATTAACAATATATTCATAGAGCGATTGAGT 3776
QY 109 ----- 109
Db 3777 TTGGACTGTGCTTCTTTGGACAAAGCCCGGGAAGTTGTTCTCTCCATTGCTAG 3836
QY 109 ----- 109
Db 3837 AAAAAATAGAACAGTTACAACTCAAGTGCACCACTGAATGAATAATGGGTCAACTCTGTTAA 3896
QY 109 ----- 109
Db 3897 TAAGACCAACTGTACTTTCATAAAACAGGGAATATCATATATCTGCAACCAACAGG 3956

QY 110 -----ValProPheTyr 113
Db 3957 AAAAGTACAGAGCTGCACTCTTACAGTTATTTTCTCTTTCATGTTTCAGTGCCATTTCTGC 4016
QY 114 GlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMet 133
|||:|||||
Db 4017 GGGGCTGCTATTCACAGCACTATTAGCAATGCAACAATCATGACTATTGATACAGAGATG 4076
QY 134 MetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyr 153
|||:|||||
Db 4077 ATGGTGGGGCTGCCCATTAATCTGCGATGCGAGGAGAGAGCGGAAGTGATGAGTAC 4136
QY 154 ArgGluLysArgLysArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAla 173
|||:|||||
Db 4137 AGGGAAGAAGAGAGAGCGGGTGCTATGCAAGCAATCCGCTACGAGTCCAGAAAGCT 4196
QY 174 TyrAlaGluLeuArgProArgValAsnGlyArgPheValLys 187
|||:|||||
Db 4197 TACGCCGAGCTCAGGCCACGGGTCAATGGCTGCTTTGTCAAG 4238

RESULT 12

ADSL9586
ID ADS19586 standard; DNA; 3454 BP.

AC ADS19586;

DT 30-DEC-2004 (first entry)

XX Langdon (tetraploid) wheat ZCCT2 genomic DNA.

XX Wild emmer wheat; ds; APETALAI; API; vernalisation; flowering; ZCCT1;
KW ZCCT2; vrn1; vrn2; CarG box; plant; gene.

XX Triticum turgidum; subsp. dicoccoides.

XX US2004205848-A1.

XX 14-OCT-2004.

XX 26-NOV-2003; 2003US-00723947.

XX 11-APR-2003; 2003US-00412137.

XX (REGC) UNIV CALIFORNIA.

XX Dubcovsky J, Yan L, Loukoianov A;

XX WPI; 2004-728059/71.

XX P-PSDB; ADS19588.

XX New recombinant ZCCT1 protein coding sequence useful for altering a
plant's (e.g., wheat, barley, rye, oats, or forage grasses) response to
vernalization or flowering times.

XX Disclosure; SEQ ID NO 84; 115pp; English.

XX The invention relates to a recombinant ZCCT1 protein (zn finger and CCT
domain protein) coding sequence comprising a nucleic acid that hybridises
to the barley ZCCT1 cDNA appearing as ADS19577. The patent also discloses
the identification of to genes, vrn1 identified as API (APETALAI) and
vrn2 identified as ZCCT1 controlling vernalisation of flowering in
temperate grasses. ZCCT1 also has a duplicate gene ZCCT2, all three genes
have been localised to chromosome 5a of one grained wheat, Triticum
monococcum. ZCCT1 is the repressor of API whose promoter contains a
binding site for ZCCT1 termed the CarG box. Also included are a vector
comprising the recombinant ZCCT1 protein coding sequence above, a cell
comprising the vector, a transgenic plant comprising the recombinant
ZCCT1 protein coding sequence above (or a genetic construct that inhibits
ZCCT1 repression of API), a seed from the transgenic plant, a method for
altering a plant's response to vernalisation and a molecular marker for
vrn2 derived from ADS19577. The genetic construct is an interference RNA
construct (RNAi) that inhibits ZCCT1 activity and comprises an antisense

CC construct that inhibits ZCCT1 activity, a nucleic acid sequence encoding
 CC a repression defective ZCCT1 protein operably linked to a promoter or a
 CC nucleic acid sequence encoding a DNA binding defective ZCCT1 protein
 CC operably linked to a promoter, the present sequence is a plant ZCCT
 CC genomic DNA sequence.

XX
 SQ Sequence 3454 BP; 962 A; 796 C; 716 G; 980 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.99e-39 Length: 3454
 Score: 538.00 Matches: 145
 Percent Similarity: 28.5% Conservative: 12
 Best Local Similarity: 26.4% Mismatches: 26
 Query Match: 51.3% Indels: 367
 DB: 13 Gaps: 5

US-10-723-947-77 (1-187) x ADS19586 (1-3454)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
 DB 1243 ATGCCCATGTCATCGGTTGTGGCGGGAAGGACTGCCGCCACCATGATCTCGCC 1302
 QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
 DB 1303 GTT-----CTTCAGCATCAGGAACACACCGCTCGCGGAGTACCATCTCTTCCAC 1353
 QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 60
 DB 1354 CAAGGC---CACCAACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 1410
 QY 61 ProAsp---AsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 79
 DB 1411 CGTTCAGCAATTGCCACCACTCCAGATCATGACCAACACCGGTTTCATGAACAGCAGCT 1470
 QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlyGlyGlyGlyGly 99
 DB 1471 GCAGGGAACAGCAGCAGGCTCAGCTGGAGGTAGACGCGGCGGCCCAACCAATGGCTC 1530
 QY 100 LeuValGlnProAlaArg----- 106
 DB 1531 CTGCTGACGACCGCAGCGCAGCGCAAGAACCAACCATCGTAGTACTACTGCTTAATTG 1590
 QY 106 ----- 106
 DB 1591 TTCAGCTCTGCGGATCGCTGGGCTCTCTTAACAAAGTTCCTTTTACGTAATCT 1650
 QY 106 ----- 106
 DB 1651 CCATCTACTCCCCCCCCCCCCCCCCCGGCATCTCAAAAAAGTTAGCGCCATGTAAAC 1710
 QY 107 -AlaHisIle----- 109
 DB 1711 AGCTCATATATCTGTCACGTAATCTGTTAATTATGCTGTTGAATATAATCTCCCAAG 1770
 QY 109 ----- 109
 DB 1771 GCAGAGTGTGTTGTTGTTGATCAGTTGATGATGATGATGATGATGATGATGATGATG 1830
 QY 109 ----- 109
 DB 1831 ACACATACATCTATTTCATTTTATTTGACTAACAAGGTAATCAGTTAATCTCTTTATG 1890
 QY 109 ----- 109
 DB 1891 GGAACAAGCAATACATATGTCACGCTTCATGTTAATTCCTTGACAAAGTTTGTGAAT 1950
 QY 109 ----- 109
 DB 1951 GGACAATATATATCTGAGTACAGTGCACCATCTTTTTCATTTTATGTTGTTATGAA 2010
 QY 109 ----- 109
 DB 2011 TTTTAGTGTATTTTGTATTTAAATTTCTTAAGCTTGTTTGTAAAGCTTATAGCTC 2070

QY 109 ----- 109
 DB 2071 AAGTATAACAGATACTACTCTCCCATTAATGCTTCGTTAGTGGCGGGTATCAATCTACC 2130
 QY 109 ----- 109
 DB 2131 GAGTTTCATAAAACTGATCGAAATCAGATCCAAAAACAGACAAAAACCTCAGAAATAGAA 2190
 QY 109 ----- 109
 DB 2191 CAAGATCTTGTGTTAATTAGTTTGACACAGGAATTTGCCTTAATTAATCTTCTATCAA 2250
 QY 109 ----- 109
 DB 2251 TCTTATGAAGATGGTATGTTTCTCACAATGATGGTATCCAGATCACAATTTGTCACGAGT 2310
 QY 109 ----- 109
 DB 2311 TAAACATTTTAGCAATTCATAAAACCGTGCACAGATGTACAGGGCTACGCGTATGCACA 2370
 QY 109 ----- 109
 DB 2371 TACATAATACACCTAATTAACACATATATTCATAGAGCATTTGAGTTTGGACTGTGCGCT 2430
 QY 109 ----- 109
 DB 2431 TCTTTGGACAAAGGCCCGGGAAGTTGTTCTCTCCATTTCTAGAAAAATAGAAACAGT 2490
 QY 109 ----- 109
 DB 2491 TACAATCAAGTCCACCACTGATGAATGAATGGGTCAATCTCGTTTAATAGAGACCAACTG 2550
 QY 109 ----- 109
 DB 2551 TACTTTCATAAACAGGGAATATCATGTACATATCTGCAACCCACAGGAAAAAGTACAGAACT 2610
 QY 110 -----ValProPheTyrGlyGlyAlaPheTh 118
 DB 2611 GCATCTTACGATTATTTCTCTTCATGTTCCAGTGCCCATTTGCGGGGCTGCATTTCAC 2670
 QY 118 rAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAl 138
 DB 2671 CAGCACTATTAGCAATGCACCATCATGACTATTGATACAGAGATGATGTTGGGGCTGC 2730
 QY 138 aHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLy 158
 DB 2731 CCATAATCTGACGATGCGAGGAGAGAGAGGCGAAGGTGATGAGGTACAGGAGAGAGAGAA 2790
 QY 158 sArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuAr 178
 DB 2791 GAGCGGGTGTATGACAAAGCAATCCGCTATGATCCAGAAAGCTTACGCGAGCTCAG 2850
 QY 178 gProArgValAsnGlyArgPheValLys 187
 DB 2851 GCCACGGGTCAATGCGCGCTTTGTCAAG 2878

RESULT 13

ADS16783
 ID ADS16783 standard; cDNA; 1078 BP.

XX ADS16783;

AC ADS16783;
 DT 16-DEC-2004 (first entry)

XX Lhd4-related Oryza sativa cDNA sequence SeqID5.
 DE Lhd4; plant flowering; flowering time; efficient development;

XX Lhd4; plant flowering; flowering time; efficient development;
 KW rice growth; gene; ss.

XX Oryza sativa.
 OS

XX WO2004081210-A1.
 PN

XX 23-SEP-2004.
XX
XX
XX PF 10-MAR-2004; 2004WO-JP003122.
XX PR 10-MAR-2003; 2003JP-00063960.
XX
XX (PLAN-) PLANT GENOME CENT CO LTD.
XX PA (PLAN-) PLANT FUNCTIONAL GENOMICS CO LTD.
XX
XX PI Minobe Y, Monna L, Kitazawa N, Maehara Y, Masuda H, Yano M;
XX
XX WPI; 2004-677545/66.
XX P-PSDB; ADS16784.
XX
XX New gene Lhd4 encoding a protein capable of delaying flowering in a
XX PT plant, useful for controlling flowering time in rice.
XX
XX PS Example 1; SEQ ID NO 5; 124pp; Japanese.
XX
XX This invention relates to a novel DNA, designated Lhd4 and encoding a
XX CC protein capable of delaying flowering in a plant. The invention is useful
XX CC for delaying flowering of a plant, which comprises expressing the novel
XX CC DNA within the cells of a plant, such as rice. The Lhd4 protein enables
XX CC control of flowering time of a plant, such as rice, thus causing
XX CC efficient development and growth of an excellent variety. The present
XX CC sequence is that of an Oryza sativa cDNA which was used in the
XX CC exemplification of the invention.
XX
XX SQ Sequence 1078 BP; 224 A; 309 C; 317 G; 228 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: Length: 2,96e-14 1078
XX Score: 258.00 Matches: 84
XX Percent Similarity: 40.6% Conservative: 19
XX Best Local Similarity: 33.1% Mismatches: 61
XX Query Match: 24.6% Indels: 90
XX DB: 13 Gaps: 14

US-10-723-947-77 (1-187) x ADS16783 (1-1078)

QY 1 MetSerMet-----SerCysGlyLeuCysGlyAlaAsnAsn-----12
DB 216 ATGTCGATGGACACAGCCGAGAGAGATGTGGCGCCGCGCAGCGTGGCGGC 275
QY 13 ---CysProArgLeuMetValSerProIleHisHisHisHisHisGlnGluHis 31
DB 276 TGTGTGTCCTCCG-----CATGCCACGATGATGAT 305
QY 32 -----GlnLeuCys-----34
DB 306 GGATTCCTCTGCTTCTCCGCGAGTGGTGGCGGATCGCGCCCGCCGCGCAGCG 365
QY 35 -----GluTyrGlnPhePheAlaHisGlyAsnHisHisHisHisHisGlySerAla 52
DB 366 GTGCACGAGTTCAGTTCCTC-----GGCAACGACGGCGCGGCGACGCGCGAGAGC 419
QY 53 Ala-----AspTyrProValProProPro-----ProAspAsnPhe 64
DB 420 GTGGCTGGCTGTTCGATGACTACCGCGCGCTGCTCCCGCGCGCGGATG 479
QY 65 AspHisArgArgThrTrpThrArgProPhe-----74
DB 480 CATATCGGACGCG-----CGGTACGACGGCGTGTGGCGCGCGCTGCTGTTC 530
QY 75 ---HisGluThrAlaAlaAlaGlyAsnSerArgLeuThrLeuGluVal-----90
DB 531 AGGAGGAACACCGCGCGCGCGG-----CTCAGTTCGACGTTCCTTCGCGC 578
QY 91 -----GlyAlaGlyGlyGlyHisMetAla 98
DB 579 GAACGCCCGACCTGACGCGCGCGGCTCGGCTCGGCGCGCGCGCGCGGAC-----632

QY 99 HisLeuValGlnProProAlaArgAlaHisIleValProPheTyrGlyGlyAlaPheThr 118
DB 633 -----GCCGAGCGCGCGCCACCATCATGTATTTGGGAGCAGCTTCACT 686
QY 119 AsnThrIleSerAsn-----GluAlaIleMetThrIleAspThrGluMet 133
DB 687 GACGAGCGAGCTCGATGCCCAAGAGAGATGGTGGCGCCCATGCCGATATGGGAGAGC 746
QY 134 MetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyr 153
DB 747 TTGAACCCCAACACACGCTGTGGCGCAATGGTGGAGAGCGGAGCGCAAGCTGATGAGGTAC 806
QY 154 ArgGluLysArgLysArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAla 173
DB 807 AAGGAGAGAGAGAGAGAGGTGTACGAGAGCAAAATCCGGTACGCGTCCAGAAAGCC 866
QY 174 TyrAlaGluLeuArgProArgValAsnGlyArgPheValLys 187
DB 867 TATGCCGAGATGAGGCCCGCGAGTGAGAGTCTGCTTCCGCCAA 908

RESULT 14
ADS16786
ID ADS16786 standard; cDNA; 1078 BP.
XX
XX AC ADS16786;
XX
XX DT 16-DEC-2004 (first entry)
XX
XX DE Lhd4-related Oryza sativa cDNA sequence SeqID8.
XX
XX KW Lhd4; plant flowering; flowering time; efficient development;
XX KW rice growth; gene; ss.
XX
XX OS Oryza sativa.
XX
XX PN WO2004081210-A1.
XX
XX PD 23-SEP-2004.
XX
XX PF 10-MAR-2004; 2004WO-JP003122.
XX
XX PR 10-MAR-2003; 2003JP-00063960.
XX
XX PA (PLAN-) PLANT GENOME CENT CO LTD.
XX PA (PLAN-) PLANT FUNCTIONAL GENOMICS CO LTD.
XX
XX PI Minobe Y, Monna L, Kitazawa N, Maehara Y, Masuda H, Yano M;
XX
XX WPI; 2004-677545/66.
XX P-PSDB; ADS16787.
XX
XX New gene Lhd4 encoding a protein capable of delaying flowering in a
XX PT plant, useful for controlling flowering time in rice.
XX
XX PS Claim 4; SEQ ID NO 8; 124pp; Japanese.
XX
XX This invention relates to a novel DNA, designated Lhd4 and encoding a
XX CC protein capable of delaying flowering in a plant. The invention is useful
XX CC for delaying flowering of a plant, which comprises expressing the novel
XX CC DNA within the cells of a plant, such as rice. The Lhd4 protein enables
XX CC control of flowering time of a plant, such as rice, thus causing
XX CC efficient development and growth of an excellent variety. The present
XX CC sequence is an Oryza sativa cDNA sequence which is claimed in the
XX CC specification.
XX
XX SQ Sequence 1078 BP; 224 A; 309 C; 316 G; 229 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: Length: 5.6e-14 1078
XX Score: 255.00 Matches: 83
XX Percent Similarity: 40.6% Conservative: 20
XX Best Local Similarity: 32.7% Mismatches: 61
XX Query Match: 24.3% Indels: 90

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model:

Run on: February 23, 2006, 10:36:58 ; Search time 4542 Seconds
(without alignments)
2340.318 Million cell updates/sec

Title: US-10-723-947-77

Perfect score: 1048

Sequence: 1 MSMSGCLGANNCPRLMVSP.....YESRKAYAEPRVNGRFVK 187

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB spool/US10723947/runat_23022006_085357_16179/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs07
-USER=US10723947 @CGN_1_1_4939 @runat_23022006_085357_16179 -NCPU=6 -ICPU=3
-NO_WMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*
1: gb.ba.*
2: gb.in.*
3: gb.env.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pr.*
9: gb.ro.*
10: gb.sts.*
11: gb.sy.*
12: gb.un.*
13: gb.vi.*
14: gb.htg.*
15: gb.pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1048	100.0	792 15	AY485969 Triticum
2	1048	100.0	850 15	AY485963 Triticum
3	1043	99.5	850 15	AY485965 Triticum

	4	1043	99.5	850	15	AY485966	Triticum
	5	1043	99.5	850	15	AY485968	Triticum
	6	1039	99.1	850	15	AY485967	Triticum
	7	1018.5	97.2	847	15	AY485964	Triticum
C	8	816	77.9	110000	15	AY485644_3	Continuation (4 of
	9	730.5	69.7	712	15	AY485975	AY485975 Triticum
	10	730.5	69.7	712	15	AY485976	AY485976 Triticum
	11	670.5	64.0	2078	15	AY485979	AY485979 Triticum
	12	590	56.3	1985	15	AY485977	AY485977 Hordeum v
	13	569	54.3	2064	15	AY485978	AY485978 Hordeum v
C	14	547.5	52.2	110000	15	AY485644_2	Continuation (3 of
	15	538	51.3	1790	15	AY485980	AY485980 Triticum
	16	260	24.8	264	15	AY687931	AY687931 Hordeum v
	17	247.5	23.6	1258	15	AK109732	AK109732 Oryza sat
	18	207	19.8	1068	6	CQ804432	Sequence
	19	207	19.8	1099	15	AY114006	AY114006 Arabidops
	20	207	19.8	1305	15	AY057632	AY057632 Arabidops
	21	207	19.8	1377	15	AY088432	AY088432 Arabidops
	22	207	19.8	1427	15	AY080747	AY080747 Arabidops
C	23	200.5	19.1	110000	15	AP008216_215	Continuation (216
	24	200.5	19.1	144191	15	AC079874	AC079874 Oryza sat
C	25	200.5	19.1	300029	15	AE017119	AE017119 Oryza sat
	26	197	18.8	1345	15	BT013260	Lycopersi
	27	195.5	18.7	110000	15	AP008208_240	Continuation (241
	28	195.5	18.7	125426	15	AP004063	Continuation (241
	29	194	18.5	1386	15	AK100097	Oryza sat
	30	194	18.5	1388	15	AK058536	Oryza sat
	31	193	18.4	1056	15	AY082963	Hordeum v
	32	191.5	18.3	50700	15	AB018118	Arabidops
	33	190.5	18.2	1324	15	AY082962	Hordeum v
	34	190.5	18.2	1455	15	AY082961	Hordeum v
	35	188.5	18.0	110000	15	AP008213_091	Continuation (92 o
C	36	188.5	18.0	150554	15	AP005307	AP005307 Oryza sat
	37	188	17.9	1101	6	AS0834	Sequence 7
	38	188	17.9	1101	6	AR099794	AR099794 Sequence
	39	187.5	17.9	944	15	AY082965	Hordeum v
	40	187	17.8	1163	15	AY082960	Hordeum v
	41	185.5	17.7	1370	15	AK109630	Oryza sat
	42	183	17.5	1060	15	AY082958	Hordeum v
	43	182.5	17.4	966	15	AY496442	Brassica
	44	182.5	17.4	1085	15	AF490474	Hordeum v
	45	182	17.4	966	15	AY356370	Brassica

ALIGNMENTS

RESULT 1	AY485969	792 bp	mRNA	linear	PLN 17-MAR-2004
LOCUS	Triticum monococcum cultivar G3116 ZCCT1 (VRN2)	mRNA	complete cds.		
DEFINITION	AY485969				
ACCESSION	AY485969.1	GI:45390705			
VERSION	AY485969.1	GI:45390705			
KEYWORDS	Triticum monococcum				
SOURCE	Triticum monococcum				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
REFERENCE	1 (bases 1 to 792)				
AUTHORS	SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.				
TITLE	The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by				
JOURNAL	Vernalization				
PUBMED	Science 303 (5664), 1640-1644 (2004)				
REFERENCE	2 (bases 1 to 792)				
AUTHORS	Van, L., Loukoianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,				
TITLE	SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.				
JOURNAL	The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by				
PUBMED	Science 303 (5664), 1640-1644 (2004)				
REFERENCE	2 (bases 1 to 792)				
AUTHORS	Van, L., Loukoianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,				
TITLE	SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.				
JOURNAL	Submitted (20-NOV-2003) Agronomy and Range Science, University of				
PUBMED	California, One Shields Avenue, Davis, CA 95616, USA				
REFERENCE	Location/Qualifiers				
source	1. .792				

QY 81 GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHisLeu 100
 Db 336 GGGAAACAGCAGCAGGCTCAGCTGGAGTGGCGCGAGCGCCACACATGGCTCACCTA 395
 QY 101 ValGlnProProAlaAlaGlnHisLeuValProPheTyrGlyGlyAlaPheThrAsnThr 120
 Db 396 GTGACGCCACCGCAAGAGCCACATCGTGCCATTTTACGGAGTGCAATCCACCAACT 455
 QY 121 IleSerAsnGluAlaLeuMetThrIleAspThrGluMetMetValGlyProAlaHisTyr 140
 Db 456 ATTAGCAATGAAGCAATCATGACTATTCACACAGATATGCTGGGGCTGCCCATTTAT 515
 QY 141 ProThrMetGlnGluAlaAlaLysValMetArgTyrArgGlnLysArgLysArgArg 160
 Db 516 CCCACAATCAGAGAGCAGCAGGAGGTGATGAGGTATAGGAGAGAGAGAGAGCGG 575
 QY 161 ArgTyrAspGlyGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180
 Db 576 CGCTATGACAAGCAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGCTCGGCCACGG 635
 QY 181 ValAsnGlyArgPheValLys 187
 Db 636 GTCAACGGCGCTTTGTCAAG 656
 RESULT 3
 Locus AY485965 850 bp mRNA linear PLN 17-MAR-2004
 DEFINITION Triticum monococcum cultivar PI272561 ZCCT1 (VRN2) mRNA, complete cds.
 ACCESSION AY485965
 VERSION AY485965.1 GI:45390685
 KEYWORDS Triticum monococcum
 SOURCE Triticum monococcum
 ORGANISM Triticum monococcum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 850)
 Yan, L., Loukoianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
 SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
 The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
 Vernalization
 Science 303 (5664), 1640-1644 (2004)
 15016992
 2 (bases 1 to 850)
 Yan, L., Loukoianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
 SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
 Submitted (20-NOV-2003) Agronomy and Range Science, University of
 California, One Shields Avenue, Davis, CA 95616, USA
 Location/Qualifiers
 1..850
 /organism="Triticum monococcum"
 /mol_type="mRNA"
 /cultivar="PI272561"
 /db_xref="taxon:4568"
 /note="winter line"
 1..850
 /gene="VRN2"
 96..737
 /gene="VRN2"
 /note="contains CCT domain similar to Arabidopsis constant
 domains"
 /codon_start=1
 /product="ZCCT1"
 /protein_id="AA560237.1"
 /db_xref="GI:45390686"
 /translation="MSMSGCLGANNCPRLMVSPPIHHHHHHQHQLCEYQFAHGNH
 HHHHGSAADYVPVPPPNDFHRRTRPFFHETAAGNSRLTLEVGAGGQMAHLVQ
 PPARAHYVFFHGAFNTISNAINTIDTMMVGPATPTWOERAAKVMYREKKRR
 RYDKQIRYESRKAYAEAPRVNCRFKVPEAMASPSPYDPSKLHLGWR"
 ORIGIN

Alignment Scores:
 Pred. No.: 1,9e-68 Length: 850
 Score: 1043.00 Matches: 186
 Percent Similarity: 100.0% Conservative: 1
 Best Local Similarity: 99.5% Mismatches: 0
 Query Match: 99.5% Indels: 0
 DB: 15 Gaps: 0
 US-10-723-947-77 (1-187) x AY485965 (1-850)
 QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAlaAsnAsnCysProArgLeuMetValSerPro 20
 Db 96 ATGTCATGTCATGCGGTTTGTGGCGCGCAACAACATGCCCCGCTCATGCTCTCGCCC 155
 QY 21 IleHisHisHisHisHisHisHisGlnGlnHisGlnLeuCysGluTyrGlnPhePheAla 40
 Db 156 ATTCAACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 215
 QY 41 HisGlyAsnHisHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60
 Db 216 CATGGCAACCCACCACCACCACCACCACCACCACCACCACCACCACCACCACCACC 275
 QY 61 ProAspAsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAlaAla 80
 Db 276 CCAGACAACTTCGACCAACCGCAGAACATGGACCAACCATTTTCATGAAACAGACGGCA 335
 QY 81 GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHisLeu 100
 Db 336 GGGAAACAGCAGCAGGCTCAGCTGGAGTGGCGCGAGCGCCACACATGGCTCACCTA 395
 QY 101 ValGlnProProAlaAlaHisMetThrIleAspThrGluMetMetValGlyProAlaHisTyr 140
 Db 396 GTGACGCCACCGCAAGAGCCACATCGTGCTGGAGTGGCGCGAGAGTGCAATCCACCACT 455
 QY 121 IleSerAsnGluAlaAlaMetThrIleAspThrGluMetMetValGlyProAlaHisTyr 160
 Db 456 ATTAGCAATGAAGCAATCATGACTATTCACACAGATATGCTGGGGCTGCCCATTTAT 515
 QY 141 ProThrMetGlnGluAlaAlaLysValMetArgTyrArgGlnLysArgLysArgArg 180
 Db 516 CCCACAATCAGAGAGCAGCAGGAGGTGATGAGGTATAGGAGAGAGAGAGAGCGG 575
 QY 161 ArgTyrAspGlyGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180
 Db 576 CGCTATGACAAGCAATCCGATACGAGTCCAGAAAAGCTTACGCTGAGCTTCGGCCACGG 635
 QY 181 ValAsnGlyArgPheValLys 187
 Db 636 GTCAACGGCGCTTTGTCAAG 656
 RESULT 4
 Locus AY485966 850 bp mRNA linear PLN 17-MAR-2004
 DEFINITION Triticum monococcum cultivar PI573529 ZCCT1 (VRN2) mRNA, complete cds.
 ACCESSION AY485966
 VERSION AY485966.1 GI:45390690
 KEYWORDS Triticum monococcum
 SOURCE Triticum monococcum
 ORGANISM Triticum monococcum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Poideae; Triticeae; Triticum.
 1 (bases 1 to 850)
 Yan, L., Loukoianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
 SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
 The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
 Vernalization
 Science 303 (5664), 1640-1644 (2004)
 15016992
 2 (bases 1 to 850)
 Yan, L., Loukoianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
 SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.


```

HHHHSRADYVPVPPPPNDHRRRTWTRPPTAAAGNSRLTLEVAGAGSOMAHLYO
PARAHIVDPHCGAATNTISALIMTIDTEMVUGPAHYPTQBRRAKMYRKRKR
RYDKQIRYESRIAYALRFRVNGRFVKVPEAMASPPSPASPYDFSKULHGWFR"

ORIGIN
Alignment Scores:
Pred. No.: 3.75e-68 Length: 850
Score: 1039.00 Matches: 185
Percent Similarity: 100.0% Conservative: 2
Best Local Similarity: 98.9% Mismatches: 0
Query Match: 99.1% Indels: 0
DB: 15 Gaps: 0

US-10-723-947-77 (1-187) x AY485967 (1-850)
QY 1 MetSerMetSerCysGlyLeuGlyAlaAsnAsnCyseProArgLeuMetValSerPro 20
DB 96 ATGTCATCATCGGTTTGTGCGCGCCAACTGCGCGCCTCATGGTCTCGCCC 155
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
DB 156 ATTACCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 215
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 60
DB 216 CATGCAACCCACCACCACCACCACCACCACCACCACCACCACCACCACCACC 275
QY 61 ProAspAsnPhaAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 80
DB 276 CCAGACAACTTCGACCCAGCAACATGAGCCAGACCATTTTCATGAAACAGCAG 335
QY 81 GlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlyGlyGlyGlyGlyGly 100
DB 336 GGGAAACAGCAGCAGGCTCACGCTGGAGGTGGCGCGCGCGCGCGCGCGCGCTA 395
QY 101 ValGlnProProAlaArgAlaHisHisHisHisHisHisHisHisHisHisHis 120
DB 396 GTGCGACCCACCGGCAAGAGCCACATCTGTCGCAATTCACGAGGTGCATTC 455
QY 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHis 140
DB 456 ATTAGCAATGAAGCAATCATGACTATTGACACAGAGATGATGGTGGCGCTTAT 515
QY 141 ProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgArg 160
DB 516 CCACAATGCAGAGAGAGCAGCAAGGTGATGAGGTATAGGAGAGAGAGAGCGG 575
QY 161 ArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaLysAlaLysAlaLys 180
DB 576 CGCTATGACAGCAATTCGATACGATCCAGATCCAGAAAGCTTACGCTGAGCT 635
QY 181 ValAsnGlyArgPheValLys 187
DB 636 GTCAACGGCGGCTTGTCAAG 656

RESULT 7
AY485964 847 bp mRNA linear PLN 17-MAR-2004
LOCUS Triticum monococcum cultivar PI221413 ZCCT1 (VRN2) mRNA, complete
DEFINITION cds.
ACCESSION AY485964
VERSION AY485964.1 GI:45390680
KEYWORDS Triticum monococcum
ORGANISM Triticum monococcum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 847)
AUTHORS Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization

61 ProAspAsnPhaAspHisArgArgThrTrpThrArgProPheHisGluThrAlaAla 80
276 CCAGACAACTTCGACCCAGCAACATGAGCCAGACCATTTTCATGAAACAGCAGCGCA 335
81 GlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlyGlyGlyGlyGlyGly 100
336 GGGAAACAGCAGCAGGCTCACGCTGGAGGTGGCGCGCGCGCGCGCGCGCTA 395
101 ValGlnProProAlaArgAlaHisHisHisHisHisHisHisHisHisHisHis 120
396 GTGCGACCCACCGGCAAGAGCCACATCTGTCGCAATTCACGAGGTGCATTCACA 455
121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHis 140
456 ATTAGCAATGAAGCAATCATGACTATTGACACAGAGATGATGGTGGCGCTTAT 515
141 ProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgArg 160
516 CCACAATGCAGAGAGAGCAGCAAGGTGATGAGGTATAGGAGAGAGAGAGCGG 575
161 ArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaLysAlaLysAlaLys 180
576 CGCTATGACAGCAATTCGATACGATCCAGATCCAGAAAGCTTACGCTGAGCTT 635
181 ValAsnGlyArgPheValLys 187
636 GTCAACGGCGGCTTGTCAAG 656

RESULT 6
AY485967 850 bp mRNA linear PLN 17-MAR-2004
LOCUS Triticum monococcum cultivar PI221413 ZCCT1 (VRN2) mRNA, complete
DEFINITION cds.
ACCESSION AY485967
VERSION AY485967.1 GI:45390695
KEYWORDS Triticum monococcum
ORGANISM Triticum monococcum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 850)
AUTHORS Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization
JOURNAL Science 303 (5664), 1640-1644 (2004)
PUBMED 15016992
REFERENCE 2 (bases 1 to 850)
AUTHORS Yan, L., Loukoianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA
FEATURES
source
1..850
/organism="Triticum monococcum"
/mol_type="mRNA"
/cultivar="PI221413"
/db_xref="taxon:4568"
/notes="winter line"
1..850
/gene="VRN2"
96..737
/gene="VRN2"
/notes="contains CCT domain similar to Arabidopsis constant
domains"
/codon_start=1
/product="ZCCT1"
/protein_id="AAS60239.1"
/db_xref="GI:45390696"
/translation="MSMSGLCGANNCPRLMVSPIHHHHHHKHLQCEYQFFAHGNH"

```


Db 32204 TGTATGGGTTGTCAAATCATAGTCATACATATATATCTTATTTCTTTTGTGACCAAC 32145
QY 109 ----- 109
Db 32144 AGAAGGTAATCAGTCATACATGCACTGAAATTAGACTTGTGTGCAATACTAACTA 32085
QY 109 ----- 109
Db 32084 ACCAACTCGACCGGCACAGCTGGGGGAAGACTTTAATCAAGCTGCTAGCTAGAGCTTAT 32025
QY 109 ----- 109
Db 32024 AATATAACATATCTTTATGAGATCAAGCAATACATATGCGCTCAATCTCAACTGTGC 31965
QY 109 ----- 109
Db 31964 AATATCTATCTGAGTCCACACTTTATGTAATTAATGACAAAGTTTGTGAAATGGAC 31905
QY 109 ----- 109
Db 31904 AATATACATCTGATCGATGACCCCTTTTCTCATTTTATGCTGCTATTAATTAATGATT 31845
QY 109 ----- 109
Db 31844 GTTATTTAGTATTCAATTTTATCTTGAGCTAGTTTTCGAAAGTCTGCTAGCTCATATATA 31785
QY 109 ----- 109
Db 31784 CTGATACTACTCCACGATAGCTTGGTAGTGGCGGTGATCGATCTACCGAGTTCTAT 31725
QY 109 ----- 109
Db 31724 AMACTGATCGAGATCGGTCCAAAAGAACAAACCCATACAAATGGAAGAGATCC 31665
QY 109 ----- 109
Db 31664 TTGTTTAGTTAGTTGATGATGAGAAATGCTTAATTAGTTTACCTGCTATCAATCTTTTGA 31605
QY 109 ----- 109
Db 31604 ACATGCGATGTTCAACCCAAACGACCCAGATCAATTAATGATGAAGTTAGCGCTTTT 31545
QY 109 ----- 109
Db 31544 AAAAACTATAAACTGTATACATGATACAGGCTACACATGTACATATATACACCTA 31485
QY 109 ----- 109
Db 31484 ATTAAACGTATATTGTAGACCAATTTGTTGGACGGTGGCATCTTTGGAAAAAAA 31425
QY 109 ----- 109
Db 31424 TGCCAGAGGAGTTGTTAGCTTCCACTGTCAGAAATAGATAGTTACAATCAAGTGCACT 31365
QY 109 ----- 109
Db 31364 TCTGAATGAAATGGATCATTTTCTAGTTAATTAGAGCAATAGACTTCCATTAACA 31305
QY 109 ----- 109
Db 31304 GGGAGTATCAAGTATCTGCTACCCATAAGAAAGTACATACTGCGATCTTATGAT 31245
QY 110 ----- ValProPheTy-GlyAlaPheThrAsnThrIleSer 122
Db 31244 TATTTTCTCTTGATGTTCAAGTGCCATTTCAAGGAGTGCAATCCACACACTATTAGC 31185
QY 123 AsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThr 142
Db 31184 AATGAAGCAATCATGACTATTGACACAGAGATGATGTTGGGGCTGCCCATATATCCACA 31125
QY 143 MetGlnGluArgAlaIleValMetArgTyrArgGluLysArgLysArgAspGlyTyr 162
Db 31124 ATCAGAGAGACAGCGAAGGTGATGAGGTATAGGAGNAGAGGAGGCGGCGCTAT 31065

QY 163 AspLysGlnIleArgTyrGluSerArgLysAlaValAlaGluLeuArgProArgValAsn 182
Db 31064 GACAAGCAATCCGATAGAGTCCAGAAAGCTTAGCTGAGCTTCGGCCATGGGTCAAC 31005
QY 183 GlyArgPheValLys 187
Db 31004 GGCCGCTTTGTCAAG 30990
RESULT 9
AY485975 712 bp mRNA linear PLN 17-MAR-2004
LOCUS Triticum monococcum cultivar PI277133 ZCCT2 (VRN2) mRNA, complete
DEFINITION cds.
ACCESSION AY485975
VERSION AY485975.1 GI:45390730
KEYWORDS Triticum monococcum
SOURCE Triticum monococcum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 712)
AUTHORS Yan, L., Loukolanov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J.L., Echenique, V. and Dubcovsky, J.
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization
JOURNAL Science 303 (5664), 1640-1644 (2004)
PUBMED 15016992
REFERENCE 2 (bases 1 to 712)
AUTHORS Yan, L., Loukolanov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J.L., Echenique, V. and Dubcovsky, J.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA
FEATURES
source
1..712
/organism="Triticum monococcum"
/mol_type="mRNA"
/cultivar="PI277133"
/db_xref="taxon:4568"
/note="winter line"
1..712
/gene="VRN2"
29..667
/gene="VRN2"
/note="contains CCT domain similar to Arabidopsis constant
domains"
/codon_start=1
/product="ZCCT2"
/protein_id="AAS60247.1"
/db_xref="GI:45390731"
translation="MSMSGCGLCGAGSDCPHHMISPVLOHQHQLREYQFFTOGHHHHH
HGAADYPPPPPPSANCHRSWTTFPHETAAAGNSRLTLEVDAGQNMALLOPPA
RPRTIVPCGAATSTISNATIMTDEMAVGAHNLTMOERAKVMRYRKRRC
YDKQIRYSRKAAYELRPVNGCFVKVPEAAASSPPASPYDPSKLHLGWFO"

ORIGIN

Alignment Scores:

Pred. No.: 2,146-45 Length: 712
Score: 730.50 Matches: 144
Percent Similarity: 81.6% Conservative: 11
Best Local Similarity: 75.8% Mismatches: 28
Query Match: 69.7% Indels: 7
DB: 15 Gaps: 4

US-10-723-947-77 (1-187) x AY485975 (1-712)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
Db 29 ATGTCATGTCATGCGGTTTGTGCGCGCAAGCACTGCCCGCACCATGATCTCGCCC 88
QY 21 IleHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPheAla 40

```

Db 89 GTT-----CTTCAGCATCAGGACCAACATCGCTGCGGAGTACAGTCTTCACC 139
Qy 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60
Db 140 CAAAGGC--CACCACCAACACCAACACGCGCGCGGCGGACTACCCACCGCCACCGCCA 196
Qy 61 ProAsp---AsnPheAspHisArgArgThrTrpThrArgProPheHisGluThrAla 79
Db 197 CCGTCGCGCAATTGCCACCACTGCAGATCATGACCAACACCGCTTCATGAAACAGCAGCT 256
Qy 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHis 99
Db 257 GCAGGGAACAGCGACAGATCAGCTGGAGGTAGATGCAGGCGCGCAAAACATGGCTCAC 316
Qy 100 LeuValGlnProProAlaAlaHis-----IleValProPheTyrGlyGlyAlaPhe 117
Db 317 CTGCTGCAGCACCGCGCACGCAAGAACCAACCATCGTCCCATTCCTGCGGGGCTGCATT 376
Qy 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
Db 377 ACCAGCACTATTAGCAATCAACAATCATCATCTATTATACAGATGATGGTGGGGCT 436
Qy 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157
Db 437 GCCCATAACTGCAGATGCAGGAGAGAGAGAGAGAGAGTATGAGGTACAGGAGAGAGG 496
Qy 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
Db 497 AGAGGCGGTGTATGACAGCAATCCGCTACGATCCAGAAAGCTTACCCGAGCTC 556
Qy 178 ArgProArgValAsnGlyArgPheValLys 187
Db 557 AGGCCACGGGTCAATGGCTGCTTGTCAAG 586

RESULT 10
AY485976 712 bp mRNA linear PLN 17-MAR-2004
LOCUS Triticum monococcum cultivar Piz2561 ZCCT2 (VRN2) mRNA, complete
DEFINITION cds.
ACCESSION AY485976
VERSION AY485976.1 GI:45390733
KEYWORDS Triticum monococcum
SOURCE Triticum monococcum
ORGANISM Triticum monococcum

REFERENCE
AUTHORS Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.
The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization
JOURNAL Science 303 (5664), 1640-1644 (2004)
PUBMED 15016992
REFERENCE 2 (bases 1 to 712)
AUTHORS Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.
Direct Submission
JOURNAL Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA
FEATURES
source
1. .712
/organism="Triticum monococcum"
/mol_type="mRNA"
/cultivar="Piz2561"
/db_xref="taxon:4568"
/note="winter line"
1. .712
/gene="VRN2"
25. .667
/gene="VRN2"
/feature="contains CCT domain similar to Arabidopsis constant

gene
CDS
/feature="contains CCT domain similar to Arabidopsis constant

```

```

domains"
/codon_start=1
/product="ZCCT2"
/protein_id="AAS60248.1"
/db_xref="GI:45390734"
/tranlation="MSMSGICGASDCPHHMI SPVLOHOBHWHLREYOFFFTQGHHHH
HGAADYPPPPPSANCHCRSWTPPHEATAAGNSRLTLEVDAGGNMAHLLOPPA
RPRTTIPFGCAFTSTISNATIMTDEMVMGAHNHMOERAKNWKYREKRRC
YDKQIRYESRKAYAEALPRVNGCFVKVPEAAAASSPPASYPDPKSLHLGWFQ"

ORIGIN
Alignment Scores:
Pred. No.: 2,148-45 Length: 712
Score: 730.50 Matches: 144
Percent Similarity: 81.6% Conservative: 11
Best Local Similarity: 75.8% Mismatches: 28
Query Match: 69.7% Indels: 7
DB: 15 Gaps: 4

US-10-723-947-77 (1-187) x AY485976 (1-712)
Qy 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20
Db 29 ATGTCATGTCATCGGTTTGTGCGCGCAAGCGACTGCCCGCACCATGATCTCGCCC 88
Qy 21 IleHisHisHisHisHisHisHisGlnGluHisGlnLeuCysGluTyrGlnPhePheAla 40
Db 89 GTT-----CTTCAGCATCAGGACCAACACTCGCTGCGGAGTACAGTCTTCACC 139
Qy 41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro 60
Db 140 CAAAGGC--CACCACCAACACCAACCGCGCGGCGGACTACCCACCGCCACCGCCA 196
Qy 61 ProAsp---AsnPheAspHisHisHisHisHisHisGlnGluHisGlnPheAla 79
Db 197 CCGTCGCGCAATTGCCACCACTGCAGATCATGAGCAACACCGCTTCATGAAACAGCAGCT 256
Qy 80 AlaGlyAsnSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHis 99
Db 257 GCAGGGAACAGCAGCAGACTCAGCTGGAGGTAGATGCAGGCGCGCAAAACATGGCTCAC 316
Qy 100 LeuValGlnProProAlaAlaHis-----IleValProPheTyrGlyGlyAlaPhe 117
Db 317 CTGCTGCAGCACCGCGCACGCAAGAACCAACCATCGTCCCATTCCTGCGGGGCTGCATT 376
Qy 118 ThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyPro 137
Db 377 ACCAGCACTATTAGCAATCAACAATCATCATCTATTATACAGATGATGGTGGGGCT 436
Qy 138 AlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArg 157
Db 437 GCCCATAACTGCAGATGCAGGAGAGAGAGAGAGAGTATGAGGTACAGGAGAGAGG 496
Qy 158 LysArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeu 177
Db 497 AGAGGCGGTGTATGACAGCAATCCGCTACGATCCAGAAAGCTTACCCGAGCTC 556
Qy 178 ArgProArgValAsnGlyArgPheValLys 187
Db 557 AGGCCACGGGTCAATGGCTGCTTGTCAAG 586

RESULT 11
AY485979 2078 bp DNA linear PLN 17-MAR-2004
LOCUS Triticum turgidum cultivar Langdon ZCCT1-Td (VRN2) gene, complete
DEFINITION cds.
ACCESSION AY485979
VERSION AY485979.1 GI:45390744
KEYWORDS Triticum turgidum
SOURCE Triticum turgidum
ORGANISM Triticum turgidum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```

REFERENCE	Pooideae; Triticeae; Triticum.	QY	109	-----	109
AUTHORS	1 (bases 1 to 2078)	Db	435	TTGCCGATGGATGGCTCCTGGCTTCCTTAAATAATCCCACTAATTTATGTCATC	494
TITLE	Yan,L., Loukoianov,A., Blechl,A., Tranquilli,G., Ramakrishna,W., SanMiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J. The wheat VRN2 Gene is a Flowering Repressor Down-Regulated by Vernalization	QY	109	-----	109
JOURNAL	Science 303 (5664), 1640-1644 (2004)	Db	495	TATACCCACTACAAAAAATAGCACCATGTAAACCATCTCATATATCTGTACATAATTTCT	554
REFERENCE	15016992	QY	109	-----	109
AUTHORS	2 (bases 1 to 2078)	Db	555	GTTAATGTACGCTGCTCAATTTCTCTGAAAAAGATATGCGGAATGGATCTTGATAT	614
TITLE	SanMiguel,P., Bennetzen,J.L., Echenique,V. and Dubcovsky,J. Direct Submission	QY	109	-----	109
JOURNAL	Submitted (20-NOV-2003) Agronomy and Range Science, University of California, One Shields Avenue, Davis, CA 95616, USA	Db	615	TCTTTAATTTTCTATGGAGGCATATATAGAGTTTGTGTTTGTATAGTTGATGCAGAT	674
FEATURES	Location/Qualifiers	QY	109	-----	109
source	1. .2078	Db	675	TGTATGGGTGTCAAAATCATCAGTCATACATATAAACTTATTTTATTTTGGACCAAC	734
	/organism="Triticum turgidum"	QY	109	-----	109
	/mol_type="genomic DNA"	Db	735	AACAAAGTAATCAGTCATACATGTCATCTGAAATTTGACTTGTGTTCAATTAACCA	794
	/cultivar="Langdon"	QY	109	-----	109
	/db_xref="taxon:4571"	Db	795	ACTCGACCGCACAGCTGGGGGAAGACTTAAATCAAGCTGCTAGCTAGAGCTTAATAA	854
	/clone="BAC 354M17"	QY	109	-----	109
	/note="winter line; tetraploid genome A"	Db	855	TAAATATCTCTTTATGGGATCAAGCAATACATATGCTCAATTTCTCACTTGCAATA	914
gene	<96..>1965	QY	109	-----	109
mRNA	/gene="VRN2"	Db	915	TCTATCTGGATCCACACTTTATGGTAATAATTGACAAAGTTTTGTGAAATGGACA	974
	join(<96..401,1651..>1965)	QY	109	-----	109
	/gene="VRN2"	Db	975	TACATCTGGATCGATGCACCTTTTCTCATTTTATGTGGTCATTATGAATTTGATGT	1034
	/product="ZCCT1-Td"	QY	109	-----	109
	join(96..401,1651..1965)	Db	1035	TATTTAGTATTTCAATTTTATCTTGAGCTAGTTTGGCAAGTCTGTAGCTCATATATA	1094
	/gene="VRN2"	QY	109	-----	109
	/codon_start=1	Db	1095	GATACTACTCCCAAGATAGCTTGGTAGTGGCGGGTATCGATCTACCGAGTTCAATA	1154
	/product="ZCCT1-Td"	QY	109	-----	109
	/protein_id="AAS60251.1"	Db	1155	AACTGATCGAGTCGGGTCCAAAAAAGAACAAACCCATACAAAAAGGAAGATCCTT	1214
	/db_xref="GI:45390745"	QY	109	-----	109
	/translation="MSMSGLCGANNCPRLMVSPPIHRRHHHOLRQHPFAQGNH HHHVPLPPANFDSRTWTFPHETAAGNSSRLTLEVGAGRPMAHLVQPARAHI VFGYGAFTNTISNAITIDTEMVGPAPHYPTMOERAAKVMRYREKRRRYDKQIR YESRKAYAEELRPVNGCFVKVPEAMASPSPPYDPSKHLGWER"	Db	1215	GTTTAGTTAGTTTGCATCAGAAAAATTGCTTAATTAGTTACTTGTCTATCAATCTTTTGA	1274
ORIGIN		QY	109	-----	109
Alignment Scores:		Db	1275	ATGGCATGTTCAACCCCAACCGGACTCAGATCAATTTATGTAGTGAAGTTACGCTTTTAA	1334
Pred. No.:	1.93e-40	QY	109	-----	109
Score:	670.50	Db	1335	AAACTCATAAACTGTATACATGTACAGGGCTACACATGTATACATATACACCTAAT	1394
Percent Similarity:	28.3%	QY	109	-----	109
Best Local Similarity:	27.8%	Db	1395	TAAAAAGTATATTCTGTAGACCAATTGTTTGTGACGGTGCACATCTTTGAAAAAATG	1454
Query Match:	64.0%	QY	109	-----	109
Indels:	424	Db	1455	AGAGGAGTTGTAGCTTCCACTGTCCAGAAATAGTAATAGTTACAATCAAGTGCATCT	1514
Gaps:	15	QY	109	-----	109
		Db	1514	-----	1514
US-10-723-947-77 (1-187) x AY485979 (1-2078)		QY	109	-----	109
1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro	20	Db	1555	AACTGATCGAGTCGGGTCCAAAAAAGAACAAACCCATACAAAAAGGAAGATCCTT	1614
96 ATGTCCATGTCATCGGTTTGTGCGGCGCAACAACTGCCGCGCTCATGTCTCGGCC	155	QY	109	-----	109
21 IleHisHisHisHisHisHisGlnGluHisGlnLeuCysGlyIleGlnPhePheAla	40	Db	1615	GTTTAGTTAGTTTGCATCAGAAAAATTGCTTAATTAGTTACTTGTCTATCAATCTTTG	1674
156 ATTTCATCTGTCATCACCATCATCAGGAGCACCAGCTCGTCAGCACCCAGTTCTT	215	QY	109	-----	109
41 HisGlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProPro	60	Db	1675	ATGGCATGTTCAACCCCAACCGGACTCAGATCAATTTATGTAGTGAAGTTACGCTTTTAA	1734
216 CAAGGCAACCAACCAACCAACCAAC-----CCAGTGCACCTGCGC	254	QY	109	-----	109
61 ProAspAsnPhaAspHisArgArgThrTTPThrArgProPheHisGluThrAlaAla	80	Db	1735	AAACTCATAAACTGTATACATGTACAGGGCTACACATGTATACATATACACCTAAT	1794
255 CCAGCAACTTCGACCATAGCAGACATGCACACCACTTTTCATGAACACGACGCTG	314	QY	109	-----	109
81 GlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis	100	Db	1795	TAAAAAGTATATTCTGTAGACCAATTGTTTGTGACGGTGCACATCTTTGAAAAAATG	1854
315 GGGACAGCAGCAGGCTCAGCTGGAGGTGGGGGAGGGCGGCGCCATGCTCACCTA	374	QY	109	-----	109
101 ValGlnProProAlaAlaHisIle-----	109	Db	1855	AGAGGAGTTGTAGCTTCCACTGTCCAGAAATAGTAATAGTTACAATCAAGTGCATCT	1914
375 GTGACGCCACCGGCAAGAGCCACATCGTAAGTAGTAGTACCGCTTAATTGTTTCT	434	QY	109	-----	109

Db 1515 AATGAAATGGATCATTTTCTAGTTAAATAGAGACCAATTAGATCTTCATAAAGAGGG 1574

QY 109 ----- 109

Db 1575 AGTATCAAGTACGTATCTGTACCTACCAAGATACATAACTCGCATCTTATGATTATT 1634

QY 110 -----ValProPheTyrGlyGlyAlaPheThrAsnThrIleSerAsnG1 124

Db 1635 TCCTCTTGATGTTACGGTGCATTTTACGGAGGTGCATTCACCAACACATATTAGCAATGA 1694

QY 124 uAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThrMetG1 144

Db 1695 AGCAATCATGACTATTGACACAGAGATGATGGTGGGCGCTGCCCATATATCCACCAATGCA 1754

QY 144 nGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgTyrAsp164

Db 1755 GGAGAGAGCAGCGAAGGTGATGAGGTATAGGAGAGAGAGAGCGCGCTATGACNA 1814

QY 164 sGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGlyAr 184

Db 1815 GCAAATCATGACAGTCCAGAAAGCTTACGCTGAGCTTCGGCCACGGGTCAACGGCTG 1874

QY 184 gPheValLys 187

Db 1875 CTTTGTCAAG 1884

RESULT 12

LOCUS AY485977

DEFINITION Hordeum vulgare cultivar Dairokkaku ZCCT-Ha (VRN2) gene, partial cds.

ACCESSION AY485977

VERSION AY485977.1 GI:45390737

KEYWORDS

SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare

REFERENCE 1 (bases 1 to 1985)

AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.

TITLE 1 (bases 1 to 1985)

AUTHORS Yan, L., Loukolanov, A., Blechl, A., Tranquillini, G., Ramakrishna, W., SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.

THE WHEAT VRN2 GENE IS A FLOWERING REPRESSOR DOWN-REGULATED BY VERNALIZATION

JOURNAL Science 303 (5664), 1640-1644 (2004)

PUBMED 15016992

REFERENCE 2 (bases 1 to 1985)

AUTHORS Yan, L., Loukolanov, A., Blechl, A., Tranquillini, G., Ramakrishna, W., SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.

DIRECT SUBMISSION

TITLE Submitted (20-NOV-2003) Agronomy and Range Science, University of California, One Shields Avenue, Davis, CA 95616, USA

JOURNAL

FEATURES

Location/Qualifiers

1..1985

/organism="Hordeum vulgare"

/mol_type="genomic DNA"

/cultiar="Dairokkaku"

/db_xref="taxon:4513"

/note="winter barley"

<336..>1985

/gene="VRN2"

join(<336..665,1677..>1985)

/gene="VRN2"

/product="ZCCT-Ha"

join(336..665,1677..>1985)

/gene="VRN2"

/codon_start=1

/product="ZCCT-Ha"

/protein_id="AAS60249.1"

/db_xref="GI:45390737"

/translation="MSMSGGLCGASNCAYHMSVLLHHHHHHEHPLHEYOFFAAGHH

HHHSAADYPPPPPPDCHHRSWTTTFFHETAAPDENSTRUTREVDAGGQHALLQP

ORIGIN

Alignment Scores:

Pred. No.: 1,67e-34 Length: 1985

Score: 590.00 Matches: 147

Percent Similarity: 29.6% Conservative: 9

Best Local Similarity: 27.9% Mismatches: 29

Query Match: 56.3% Indels: 342

DB: 15 Gaps: 4

US-10-723-947-77 (1-187) x AY485977 (1-1985)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValSerPro 20

Db 336 ATGTCCATGTCTATGGTTTGTGGCGCCAGCAACTCGCGTACCACATGATGTCGCC 395

QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40

Db 396 GTTCTTCTTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 455

QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 59

Db 456 CAAGT-----CACCAACCACACAGCGCGGCGGACTACCCACCAACCGCCA 509

QY 60 ProProAspAsnPheAspHisArgThrTrpThrArgProPheHisGluThrAlaAla 79

Db 510 CCGCCAGACATTCGCCACCACACAGATCATGGACCGCGCTTCATGAACACAGCAGT 569

QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlyHisMetAlaHis 99

Db 570 CCAGAGAACAGCAGCAGCGCTCACAGGAGGTGGACGCGAGCGGCGGCAACACATGCTCAC 629

QY 100 LeuValGlnProProAla----- 105

Db 630 CTGTGACGCCACCGCGCGCGCCGCAAGACCACTCGTGAGTAGTAGTACTACTGCTTAATT 689

QY 105 ----- 105

Db 690 TTCTATCTCTTCCGATCGATGGAGCCTGCTAACAAATAACACACTTTCTTAATTTCCAT 749

QY 105 ----- 105

Db 750 CTCAAAAAAGCTACCGCCATGTGACACAGCTCATATATATATATATATATATATATATAT 809

QY 105 ----- 105

Db 810 TATTCTGTGCTGATGTGTAATTTACCAAGCAGAAAGCTTGATTTTGTATCAGTTGATGCA 869

QY 105 ----- 105

Db 870 CAAGAATGGGCGCTCACGTCATCAGTCGCACATACTATATATATATATATATATATATAT 929

QY 105 ----- 105

Db 930 CTAAAGAGTAAGTATGTTAATTCCTTTATGGGGTCAAGCAATACATATATATATATATATAT 989

QY 105 ----- 105

Db 990 ATGTTAATTCCTTGACAAAGTTTGTGAAGTGGAATAATATATATATATATATATATATAT 1049

QY 105 ----- 105

Db 1050 ACTCTCATTTTATGTGTGTCATTATGAATTTTATTAATTTTCTGTGTAGTAGTTTGTGA 1109

QY 105 ----- 105

Db 1110 TGCTTATAGTCATATATATACTGATACTACTCTCCCAATAATTTTCCGTAGTGGTGGGTG 1169

QY 105 ----- 105

Db 1170 ATCGATCTACCTAGTTTCATAAACTTATCGAGATCAGGTCCAAAACAGACCAAAACCTCAC 1229

QY 105 ----- 105
Db 1230 GAAATGGAACAAGATCCTTTGTTAATAGTTTGCATCAGGAATATGCTTATTACTTGCT 1289
QY 105 ----- 105
Db 1290 GTCAATCTTATGAAGTGTATTTTCCTCACAATGGATCCAGTCACAAATTTGTTGATGAA 1349
QY 106 ----- Argalahisile ----- 109
Db 1350 GTTAAACAATTTTGGCAATTCATAAAACCGTCATAGATGTCGGGTACACGCACACAAG 1409
QY 109 ----- 109
Db 1410 TACATAATACACCTAGTTTAAACATATATCCATAGACAAATGAGTTGGACTATGCGCT 1469
QY 109 ----- 109
Db 1470 TCATTGGACAAAGCCCGGAAGTTGTTCTTCCATTGTTCTAAATAATAGAACAGT 1529
QY 109 ----- 109
Db 1530 TACAGTCAAGTGCAACACTGAATGAAATGGATCAAGTTTGGTTAAACAAGAGACCAACT 1589
QY 109 ----- 109
Db 1590 TATACTTCATAAACAAGGAATATCAAGTACATATCTGCTACCCACAAGAAAGTACACT 1649
QY 110 ----- -ValProPheTyrGlyGlyAlaPheThrAsnThr 120
Db 1650 TATGACTATTTCTTCTTGATGTTTCAGTGCCATTTCTGGAGAGTGCAITGCCAGCACT 1709
QY 121 IleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyr 140
Db 1710 ATTAGCAACGCAACATCATGACTATTATATACAGAAATGATGGTGGCGCTGCTATAAT 1769
QY 141 ProThrMetGlnGluAlaAlaValMetArgTyrArgGluLysArgLysArgArg 160
Db 1770 CCAACGATGCGAGGAGAGAGCGGAGGTGTAGAGGTACAGGAGAAAGAGGAGGCGG 1829
QY 161 ArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArg 180
Db 1830 CGCTATGACAGCAATTCGCTACAGTCCAGAAAGCTTAGCGCCAGCTCAGGCCACGG 1889
QY 181 ValAsnGlyArgPheValLys 187
Db 1890 GTCAATGCGCGCTTTGCCAAG 1910
RESULT 13
AY485978 2064 bp DNA linear PIN 17-WAR-2004
LOCUS Hordeum vulgare cultivar Dairokkaku ZCCT-Hb (VRN2) gene, partial
DEFINITION cds.
ACCESSION AY485978
VERSION AY485978.1 GI:45390740
KEYWORDS
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 2064)
Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.
TITLE The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
vernalization
JOURNAL Science 303 (5664), 1640-1644 (2004)
PUBMED 15016992
REFERENCE 2 (bases 1 to 2064)
Yan, L., Loukianov, A., Blechl, A., Tranquilli, G., Ramakrishna, W.,
SanMiguel, P., Bennett, J. L., Echenique, V. and Dubcovsky, J.
TITLE Direct Submission

JOURNAL

Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA

FEATURES

Location/Qualifiers
1. .2064

source

/organism="Hordeum vulgare"
/mol_type="genomic DNA"
/cultivar="Dairokkaku"
/db_xref="taxon:4513"
/note="winter barley"
<420. >2064
/gene="VRN2"
join(<420. .752,1756. >2064)
/gene="VRN2"
/product="ZCCT-Hb"
join(420. .752,1756. >2064)
/gene="VRN2"
/codon_start=1
/product="ZCCT-Hb"
/protein_id="AA560250.1"
/db_xref="GI:45390741"
/translation="MSNACGLCGASNCYPHNMSPVLLHHHHQHQRQREYQFFAQGHH
HHHGAADYPPQPPFANCHRRSWATLFHETAAPVNSTLTLEVDAGGQMAHLQ
PPAPPRATIVPFRSAFTNTISNATITIDTEMAGTAYSPTMOERAKVRYRKRK
KRRYDKQIRYESRKAYAEI RRVNGRFVKVPEAAASPPSPASPHDPSELHLGWF"

ORIGIN

Alignment Scores:

Pred. No.: 6.26e-33 Length: 2064
Score: 569.00 Matches: 146
Percent Similarity: 29.9% Conservative: 11
Best Local Similarity: 27.8% Mismatches: 29
Query Match: 54.3% Indels: 339
DB: 15 Gaps: 4

US-10-723-947-77 (1-187) x AY485978 (1-2064)

QY 1 MetSerMetSerCysGlyLeuCysGlyValAlaAsnAsnCysProArgLeuMetValSerPro 20
Db 420 ATGTCCATGGCATCGGTTTGTGGCGCCAGCAATTCGCCGTATCATCATGATGCGCCC 479
QY 21 IleHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 40
Db 480 GTTCTTCTTCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 539
QY 41 HisGlyAsnHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHisHis 59
Db 540 CAAGGT---CACCAACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCA 596
QY 60 ProProAspAsnPheAspHisAspArgThrThrThrArgProPheHisGluThrAlaAla 79
Db 597 CCGCGCGCCAAATGCCACCACCGCCAGATCATGGGCCACGCTGTTTCATGAACACGACCT 656
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlyGlnHisMetAlaHis 99
Db 657 CCAGTGATAGCACCAGCTCACAACAAGAGGTGGACGCGCGCCACACACATGCTCATC 716
QY 100 LeuValGlnProProAla-Arg----- 106
Db 717 CTGCTGACGACCGCGCGCGCCAGCAAGACCACCATCGTGAGTACTACTGCTTAATCGTTC 776
QY 106 ----- 106
Db 777 CATCTCTCCGGATCGATGTGACTCTCTTCTTAACAAAATCACATTTCTTAATTTCCATC 836
QY 106 ----- 106
Db 837 TCRAAAAAGCTAGCGCCATGTGACAGCTCATATATCTGTACATACTACTCGTTAATTT 896
QY 106 ----- 106
Db 897 ATGCTGCTGATGTAATTTTACCAAGGAGAGAAAGTTTGTGTTTGTATCAGTTGATGCAC 956
QY 106 ----- 106

Db	957	AAGACTGGATGCTCAGATCATCAGTCACACATCTATATATTTATTTCATTTTATTGAC	1016
Qy	106	-----	106
Db	1017	TAAcAGGTAATCAGTTAAITTCCTTTATGGGTCAAGCAACATATGTCcAGGCTTCATG	1076
Qy	106	-----	106
Db	1077	TTAATTCCTTTGGCAGAGTTTGTGAATAGAAGATATATATTGGGATCAATGCACCTTACC	1136
Qy	106	-----	106
Db	1137	TCITTTCTAATTTANGTGTCATTTAAGAAATTTGAATGCTATTTTGTATTTAAATTTCT	1196
Qy	106	-----	106
Db	1197	CTTGAGCTAGTGTAAAGCTTATAGCTCATATATACTGATACTACTCCCATATTGCTT	1256
Qy	106	-----	106
Db	1257	CCATAGTGGCGGTGATTGATCTACCGAGTTCATGAACCTGATCAAGATCAGGTCCAAA	1316
Qy	106	-----	106
Db	1317	ACAGGCCAAACCTCACGAATGAATTCGATCCTTGTTTAATTAGTTTGGCATCAGGA	1376
Qy	106	-----	106
Db	1377	ATTGGCTACTTAATTAATCTGCTACCAATCTTATGAAGATGGCATGTTTCCTCACAATGG	1436
Qy	106	-----	106
Db	1437	ATCCAGCTCACAATTTTTTGGTGAAGTTAAACATTTTTTAGCAATTCATAAAAGGTGCATA	1496
Qy	107	-----AlaHis-----	108
Db	1497	GATGTACAGGCTACACGTACACACGCACATATACCCCTAGTTAAACATATATGCATA	1556
Qy	108	-----	108
Db	1557	GAGCAATTGAGTTGGACAATGCGCTTCTTTGGACATAATGGCCCGGGAATTTGTTCTCT	1616
Qy	108	-----	108
Db	1617	TCCATTGCTAAAAACATAGAACAGTTAGAATCAAGTGCACCACCTGAATGAGAATGGTC	1676
Qy	108	-----	108
Db	1677	AATTTTGGTTACGAGAGACCAACTATACGTTATAAACACTGTACTCTCACCATTG	1736
Qy	109	-----IleValProPheTyrGlyAlaPheThrAsnThrIleSerAs	123
Db	1737	TTTTCTCTCGATGTTCCAGTGCCATTCGCGGAGTGCAATCCACCAACTATTAGCAA	1796
Qy	123	nGluAlaIleMetThrIleAspThrGluMetMetValGlyProAlaHisTyrProThrMe	143
Db	1797	CGCAACCATCATGACTATTGATACAGAGATGATGGCGGGACTGCCCTATATAGTCCAAAGT	1856
Qy	143	tGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLysArgArgTyrAs	163
Db	1857	GCAGGAAGAAGAACAAAGGTGATGAGTACAGGGAGAAGAGGAANGCGCGCTATGA	1916
Qy	163	pLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuArgProArgValAsnGI	183
Db	1917	CAAGCAATCCGCTACCGAGTCCAGAAAGCTTACCGCGAGCTTAGGCCACCGGTCAACGG	1976
Qy	183	YArgPheValLys 187	
Db	1977	CCGCTTTGTCAAG 1989	

WPCOMMENT

Sequence split into 5 fragments LOCUS AY485644 Accession AY485644
Fragment Name Begin End
AY485644_0 1 110000
AY485644_1 100001 210000
AY485644_2 200001 310000
AY485644_3 300001 410000
AY485644_4 400001 438828

Continuation (3 of 5) of AY485644 from base 200001 (AY485644 Triticum monococcum phosphatase transposase, phosphatidylinositol phospho..)

Alignment Scores:
Pred. No.: 1.94e-29 Length: 110000
Score: 547.50 Matches: 145
Percent Similarity: 28.2% Conservative: 11
Best Local Similarity: 26.2% Mismatches: 27
Query Match: 52.2% Indels: 371
DB: 15 Gaps: 5

US-10-723-947-77 (1-187) x AY485644_2 (1-110000)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAsnAsnCysProArgLeuMetValserPro 20
Db 55636 ATGTCCATGTCATCGGGTTTGTGGCGCAAGACTGCCGCACCATCATCTCGCCC 55577
QY 21 IleHisHishisHisHisHisHisGlnGluHisGlnLeuCysGluTyrglnPheleala 40
Db 55576 GTT-----CTTCAGCATCACGAACAACACTGGCTGGCGGAGTAGACCATTCTTCACC 55526
QY 41 HisGlyAasnHisHisHisHisHisHisGlysSerAlaAlaAspTyrPrCoValProproPro 60
Db 55525 CAAGGC---CACCAACACACACACCGCGCGCGGCGGACTACCCACCGCCACCGCCA 55469
QY 61 Proasp----AenPheaSpHisArGaRgThrTrpThrArgPropHeHisGluThrAlaAla 79
Db 55468 CCGTGCGCCAAATGGCCACCACCTGCAGATCATGGACCACACCGTTTTCATGAAACAGCAGCT 55409
QY 80 AlaGlyAasnSerSerArgLeuthrLeuCluVaiglyAlaglyGlyGlnHisMetaIehis 99
Db 55408 GCAGGGAACAGCAGCAGACTCACGCTGGAGGTAGATCGACGGCGCCAAAACATGGCTCAC 55349
QY 100 LeuValglNproProAlaArg----- 106
Db 55348 CTGCTGACGACCA CGGCA CGGCCAAGACCACCATCGTGAGTAGTACTACTGCTTAATG 55289
QY 106 ----- 106
Db 55288 TTCAGCTCTTGGCGATCGCTGGGGCTCCTTGTATAAAAAAGTTCCCTTTTACGTAATCT 55229
QY 106 ----- 106
Db 55228 CCATCTACTCCCCCCCCCCCCCCCCCCCCCCCGCCCTCCCGCATCTCAA AAAAGT 55169
QY 107 -----Alahisile----- 109
Db 55168 TAGGGCCATGAACACGCTCATATATCTGTGCACATAATTCGTAAATTTATGCTGTCACAA 55109
QY 109 ----- 109
Db 55108 TTATAATCTCCCAAGGCAGAAAGTTTGTGTTTTGTATCAGTTGTATGAACAAGAATGGGAA 55049
QY 109 ----- 109
Db 55048 CTCACATCATCAGTTACACATACATCTATTTTATTTATTTGCACTAACAAAGGTATCA 54989
QY 109 ----- 109
Db 54988 GTTAAITTCCTTTATGGGAAACAAGCAATACATATGTCCACGCCCTTCATGTTAATTCCTTGA 54929
QY 109 ----- 109
Db 54928 CAAAGTTTGTAATGGCAATATATATATCTGGATCAATGACCCCTCTTCTCTATTTAT 54869

```

QY 109 ----- 109
Db 54868 GTGGTCATTATGAATTTTAGTGTCTATTATATATTAAATTTCTCTTAAGCTTGTTTG 54809
QY 109 ----- 109
Db 54808 TAAGCTTATAGCTCATGTATAACAGATACTACTCCCATTAATTTGCTTCGTAGTGGCCGG 54749
QY 109 ----- 109
Db 54748 GTGATCAATCTACCGAGTTTCATAAACTGATCGGATCAGATCCAAACAGACCAAAACC 54689
QY 109 ----- 109
Db 54688 TCACGAATAGAAACAAGATCTCTGTTTAAATAGTTTGACACGAGAAATGCTACTTAA 54629
QY 109 ----- 109
Db 54628 TTACTTTCTATCAATCTTATGAACATGGCATGTTTCTCACAATGATGGTACCAGATCACA 54569
QY 109 ----- 109
Db 54568 ATTGTTGACGGAGTTAAACAATTTTAGCAATTCATAAAACCATGCACAGATGTACAGGGC 54509
QY 109 ----- 109
Db 54508 TAGCGGTATGCACATACATAATACACCTTAATTAACATATATTCATAGAGGATGAGT 54449
QY 109 ----- 109
Db 54448 TTGCACTGTGGCTTCTTTGGACAAAGCCCGGGAAGTTGTTCTCTTCCATTGCTAG 54389
QY 109 ----- 109
Db 54388 AAAATAGAACAGTTTACAATCAAGTGCACCACTGAATGAAATGGTCAACTCTGTTTAA 54329
QY 109 ----- 109
Db 54328 TAAGAGACCAACTGTACTTTCATAAACAGGATATCATGTACATATCTGCACCCACAGG 54269
QY 110 ----- ValProPheTyr 113
Db 54268 AAAAGTACAGAGCTGCACCTCTTACAGTTATTTCTCTCTTCATGTTTCAGGTGCCATTCGC 54209
QY 114 GlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrClnuMet 133
Db 54208 GGGGCTGCATTCCACGACCATTTAGCAATTTAGCAATTCATGACTATTGATACAGAGATG 54149
QY 134 MetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyr 153
Db 54148 ATGTTGGGGCTGCCCATTAATCTGACGATGCAGGAGAGAGAGGCGAAGGTGATGAGGTAC 54089
QY 154 ArgGluLysArgLysArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAla 173
Db 54088 AGGAGAAAGAGAGAGCGGTGCTATGACAGCAAAATCCGCTACGACTCCAGAAAAGCT 54029
QY 174 TyrAlaGluLeuArgProArgValAsnGlyArgPheValLys 187
Db 54028 TACGCCGAGCTCAGGCCCGGGTCAATGGCTGCTTTGTCAAG 53987

RESULT 15
AY485980 LOCUS AY485980 1790 bp DNA linear PLN 17-MAR-2004
DEFINITION Triticum turgidum cultivar Langdon ZCCT2-Td (VRN2) gene, complete
cds.
ACCESSION AY485980
VERSION AY485980.1 GI:45390748
KEYWORDS Triticum turgidum
SOURCE Triticum turgidum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

```

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

```

1 (bases 1 to 1790)
Yan, L., Loukianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
The Wheat VRN2 Gene Is a Flowering Repressor Down-Regulated by
Vernalization
Science 303 (5664), 1640-1644 (2004)
15016992
2 (bases 1 to 1790)
Yan, L., Loukianov, A., Blechl, A., Tranquillini, G., Ramakrishna, W.,
SanMiguel, P., Bennetzen, J.L., Echenique, V. and Dubcovsky, J.
Direct Submission
Submitted (20-NOV-2003) Agronomy and Range Science, University of
California, One Shields Avenue, Davis, CA 95616, USA
Location/Qualifiers
1. 1790
/organism="Triticum turgidum"
/mol_type="genomic DNA"
/cultivar="Langdon"
/db_xref="taxon:4571"
/clone="BAC 326E2"
/notes="winter line; tetraploid genome A"
<29..>1745
/gene="VRN2"
/join(<29..352,1431..>1745)
/gene="VRN2"
/product="ZCCT2-Td"
/join(29..352,1431..1745)
/gene="VRN2"
/codon_start=1
/product="ZCCT2-Td"
/protein_id="AAS60252.1"
/db_xref="GI:45390749"
/translation="MPMSCGLCGASDCPHNMISPVLOHQEHLRLREYOFFFTGGHHHH
HDAADTPPPPPSANCHRSWITTPHETAAAGNSRLTLEVDAGGNMAHLLOPPA
RPRTIYVPGCAFTSTISNATITIDTMMVGAHNLTMOERAKVMRYRKRKRC
YDKQIRYESKAYAEALPRVNGRFVKVPEAAASSPPASPDPSKHLGWER"

```

ORIGIN

```

Alignment Scores:
Pred. No.: 1,06e-30 Length: 1790
Score: 538.00 Matches: 145
Percent Similarity: 28.5% Conservative: 12
Best Local Similarity: 26.4% Mismatches: 26
Query Match: 51.3% Indels: 367
DB: 15 Gaps: 5

US-10-723-947-77 (1-187) x AY485980 (1-1790)

QY 1 MetSerMetSerCysGlyLeuCysGlyAlaAlaAsnAsnCysProArgLeuMetValSerPro 20
Db 29 ATGCCCATGTCATCGGGTTTGTGGCGGCGAGCGACTGCCCGCACCACCATGATCTCGCCC 88
QY 21 IleHisHisHisHisHisHisHisHisGlnGlnHisGlnLeuCysGluTyrGlnPhePheAla 40
Db 89 GTT-----CTTCAGCATCAGGAACACACACCGGCTGCGGAGTACAGTCTTCTACC 139
QY 41 HisGlyAsnHisHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro 60
Db 140 CAAGGC---CACACACACACACACACCGCGCGGCGGACTACCCACCGCCACCGCA 196
QY 61 ProAsp---AsnPheAspHisArgThrTrpThrArgProPheHisGluThrAlaAla 79
Db 197 CCGTCAGCCAATTGCCACCACTGCAGATCATGGACACACACCGTTTCATGAAACAGCAGCT 256
QY 80 AlaGlyAsnSerSerArgLeuThrLeuGluValGlyAlaGlyGlnHisMetAlaHis 99
Db 257 GCAGGGAACAGCAGCAGGCTCACGCTGGAGGTAGACGCGGCGGCAAAACATGCTCTCAC 316
QY 100 LeuValGlnProProAlaArg----- 106
Db 317 CTGCTGCAGCCACCGGACCGCCAAAGAACCAACCATCGTGTAGTAGTACTGCTTAAATTG 376
QY 106 ----- 106

```

```
Db 377 TTCCAGCTCTTGCAGATCGGTTGGGCTCTCTTCTAAACAAAGTTCCCTTTTACGTAATCT 436
Qy 106 -----
Db 437 CCATCTACTCCCGCCCCCCCCCGGCATCTCAAAAAGTTAGCGCCATGTAAAC 496
Qy 107 -AlaHisIle-----
Db 497 AGCTCATATATCTGTCACTAATCTCTGTTAAATTTATGCTGGTTGAATAATACTCCCAAG 556
Qy 109 -----
Db 557 GCAGAGTGTGTTGTTGTTGTTGATCAGTTGATGCACAAAGATGGGCACTCACATCATCGTT 616
Qy 109 -----
Db 617 ACACATACATACTTATTTTCATTTTATTGACATAACAAGTAATCAGTTAAATTCCTTTATG 676
Qy 109 -----
Db 677 GGAACAAGCAATACATATGTCACGCTTCAATGTTAAATTCCTTGACAAAGTTTGTGAAT 736
Qy 109 -----
Db 737 GGACAATATATATCTGGATCAGTGACCAATCTTTTTCATTTTATGTTGTCATTTATGAA 796
Qy 109 -----
Db 797 TTTTAGTCTATTTCATTTTAAATTTTCTTCTTAAGCTTGTTCAGCTTATAGCTC 856
Qy 109 -----
Db 857 AAGTATAACAGATACTACTCCCAATATGCTTCGATGTCGGGTGATCAATCTACC 916
Qy 109 -----
Db 917 GAGTTCATAAACTGATCGAAATCAGATCCAAAACAGACCAAAACCTCAGAAATAGAAA 976
Qy 109 -----
Db 977 CAAGATCCTTGTGTTTAAATTTAGTTTGACAGGAAATGCTACTTAATTAATTTCTATCAA 1036
Qy 109 -----
Db 1037 TCTTATGAAGATGTTGTTCTCACAATGTTGATCCAGATCACAATTTGTTGACGAGT 1096
Qy 109 -----
Db 1097 TAAACATTTTAGCAATTCATAAAACCGTGACAGATGTACAGGCTACGGGTATGCACA 1156
Qy 109 -----
Db 1157 TACATAATACACTTAATTAACATATATTATAGAGCGATTGAGTTGGACTGTGCGCT 1216
Qy 109 -----
Db 1217 TCTTTGGACAAAGCGCGGAGTTGTTCTCTTCCATTGTCTAGAAAAATAGAACAGT 1276
Qy 109 -----
Db 1277 TACAATCAAGTGCACCACTGAATGAAATGGGTCAATTTCTGTTAATAAGAGCAACTG 1336
Qy 109 -----
Db 1337 TACTTCATAACAGGAATATCATGTACATATCTGCACCCACAGAAAAAGTACAGAACT 1396
Qy 110 -----ValProPheTyrGlyAlaPheTh 118
Db 1397 GCACCTTTACGATTATTTTCCTCTTTCATGTTCCAGGTGCCATTCTCGGGGCTGCATTCCAC 1456
Qy 118 rAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMetMetValGlyProAl 138
|:::|||||
```

Search completed: February 23, 2006, 11:58:28
Job time : 4563 secs

```
Db 1457 CAGCACTATTAGCAATGCAACGATCATGACTATTGATACAGAGATGATGGTGGGGCTGC 1516
Qy 138 aHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyrArgGluLysArgLy 158
Db 1517 CCATAATCTGACGATGCAGGAGAGAGAGCGCAAGGTGATGAGGTACAGGAGAGAGAA 1576
Qy 158 sArgArgArgTyrAspLysGlnIleArgTyrGluSerArgLysAlaTyrAlaGluLeuAr 178
Db 1577 GAGGCGGTGCTATGACAAGCAAAATCCGCTATGAGTCCAGAAAAGCTTACGCCGAGCTCAG 1636
Qy 178 gProArgValAsnGlyArgPheValLys 187
Db 1637 GCCACGGGTCAATGCCCGCTTTGTCTAG 1664
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 23, 2006, 11:41:24 ; Search time 1488 Seconds
(without alignments)
267.979 Million cell updates/sec

Title: US-10-723-947-77

Perfect score: 1048

Sequence: 1 MSMSGCLGCANNCPRLMVSP.....YESRKAYAEALPRVNGRFVK 187

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB.spool/US10723947/runat_23022006.085409.16478/app_query.fasta.1
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNIT5=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs802h
-USER=US10723947 @CGN 1.1.220 @runat_23022006.085409.16478 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-XGAPOP=10 -XGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:

1: /cgn2_6/prodata/1/pubpna/US08 NEW PUB.seq.*
2: /cgn2_6/prodata/1/pubpna/US06 NEW PUB.seq.*
3: /cgn2_6/prodata/1/pubpna/US07 NEW PUB.seq.*
4: /cgn2_6/prodata/1/pubpna/PCT_NEW PUB.seq.*
5: /cgn2_6/prodata/1/pubpna/US09 NEW PUB.seq.*
6: /cgn2_6/prodata/1/pubpna/US09 NEW PUB.seq.*
7: /cgn2_6/prodata/1/pubpna/US10 NEW PUB.seq.*
8: /cgn2_6/prodata/1/pubpna/US10 NEW PUB.seq.*
9: /cgn2_6/prodata/1/pubpna/US11 NEW PUB.seq.*
10: /cgn2_6/prodata/1/pubpna/US11 NEW PUB.seq.*
11: /cgn2_6/prodata/1/pubpna/US11 NEW PUB.seq.*
12: /cgn2_6/prodata/1/pubpna/US11 NEW PUB.seq.*
13: /cgn2_6/prodata/1/pubpna/US60 NEW PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	130	12.4	200628	12	US-11-121-086-62
2	128.5	12.3	7764	12	Sequence 62, Appl Sequence 3891, Ap
3	126.5	12.1	600	12	US-11-136-527-7342
4	126.5	12.1	1428	12	US-11-136-527-3246

5	126.5	12.1	7402	8	US-10-750-185-27313	Sequence 27313, A
6	126.5	12.1	7402	8	US-10-750-623-27313	Sequence 27313, A
7	125.5	12.0	1962	12	US-11-136-527-3235	Sequence 3235, Ap
8	125	11.9	507	6	US-09-925-065A-586552	Sequence 586552, A
9	125	11.9	63693	8	US-10-995-561-13269	Sequence 13269, A
10	124.5	11.9	114801	12	US-11-121-086-22	Sequence 22, Appl
11	124	11.8	1544	12	US-11-010-239-112	Sequence 112, Appl
12	122.5	11.7	990	7	US-10-714-887-115	Sequence 115, Appl
13	122	11.6	162013	12	US-11-150-888-30	Sequence 30, Appl
14	120	11.5	1864	6	US-09-925-065A-48799	Sequence 48799, A
15	120	11.5	1864	6	US-09-925-065A-48800	Sequence 48800, A
16	120	11.5	1864	6	US-09-925-065A-48801	Sequence 48801, A
17	120	11.5	1864	6	US-09-925-065A-48802	Sequence 48802, A
18	119.5	11.4	193321	12	US-11-121-086-10	Sequence 10, Appl
19	118	11.3	558	6	US-09-925-065A-438118	Sequence 438118, A
20	117	11.2	201	12	US-11-124-367A-26036	Sequence 26036, A
21	117	11.2	1088	6	US-09-925-065A-69151	Sequence 69151, A
22	117	11.2	70513	8	US-10-995-561-13368	Sequence 13368, A
23	116.5	11.1	628	6	US-09-925-065A-640012	Sequence 640012, A
24	116.5	11.1	93112	8	US-10-995-561-13234	Sequence 13234, A
25	116	11.1	201	12	US-11-124-367A-5731	Sequence 5731, Ap
26	115.5	11.0	959	6	US-09-925-065A-88250	Sequence 88250, A
27	115.5	11.0	959	6	US-09-925-065A-88251	Sequence 88251, A
28	114.5	10.9	615	6	US-09-925-065A-433631	Sequence 433631, A
29	114	10.9	658	6	US-09-925-065A-883427	Sequence 883427, A
30	114	10.9	3457	8	US-10-750-185-50627	Sequence 50627, A
31	114	10.9	3457	8	US-10-750-623-50627	Sequence 50627, A
32	113.5	10.8	577	6	US-09-925-065A-119552	Sequence 119552, A
33	113.5	10.8	772	6	US-09-925-065A-934808	Sequence 934808, A
34	113	10.8	1475	6	US-09-925-065A-688310	Sequence 688310, A
35	112.5	10.7	600	12	US-11-136-527-6342	Sequence 6342, Ap
36	112.5	10.7	1414	12	US-11-136-527-2246	Sequence 2246, Ap
37	112.5	10.7	158468	12	US-11-112-908-56	Sequence 56, Appl
38	112.5	10.7	193789	12	US-11-112-908-55	Sequence 55, Appl
39	112	10.7	554	6	US-09-925-065A-408177	Sequence 408177, A
40	112	10.7	6497	8	US-10-821-234-839	Sequence 839, Appl
41	111.5	10.6	463	6	US-09-925-065A-213874	Sequence 213874, A
42	111.5	10.6	1662	12	US-11-136-619-3	Sequence 3, Appli
43	111	10.6	1152	7	US-10-714-887-349	Sequence 349, Appl
44	111	10.6	1189	8	US-10-055-877-29	Sequence 29, Appl
45	111	10.6	2840	12	US-11-136-527-2131	Sequence 2131, Ap

ALIGNMENTS

RESULT 1
US-11-121-086-62
; Sequence 62, Application US/1121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 62
; LENGTH: 200628
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-62

Alignment Scores:	1.57	Length:	200628
Pred. No.:	130.00	Matches:	21
Score:	57.8%	Conservative:	5
Best Local Similarity:	46.7%	Mismatches:	19
Query Match:	12.4%	Indels:	1
DB:	12	Gaps:	0


```
/ FILE REFERENCE: 031896-041000 (AM101086)
/ CURRENT APPLICATION NUMBER: US/11/136,527
/ CURRENT FILING DATE: 2005-05-25
/ PRIOR APPLICATION NUMBER: US 60/574,294
/ PRIOR FILING DATE: 2005-05-26
/ NUMBER OF SEQ ID NOS: 362830
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 3235
/ LENGTH: 1962
/ TYPE: DNA
/ ORGANISM: Rattus norvegicus
US-11-136-527-3235

Alignment Scores:
Pred. No.: 0.0298 Length: 1962
Score: 125.50 Matches: 43
Percent Similarity: 38.0% Conservative: 25
Best Local Similarity: 24.0% Mismatches: 64
Query Match: 12.0% Indels: 47
DB: 12 Gaps: 7

US-10-723-947-77 (1-187) x US-11-136-527-3235 (1-1962)

Qy 7 LeuGlyAlaAsnAsnGlyGlnGluHisGlnLeuMetValSer-----Protle 21
Db 365 CTCATCGGCTCCACCCAGTGCACACCGCTGCAGAGCTTCGACGGCTTCGCTAGTGGC 424
Qy 22 HisHisHisHisHisHisHisGlnGluHisGlnLeuGlyGluTyr----- 36
Db 425 CACCACCATCACCACACACACACCTCATCCGACCCAGCGGTACCCAGGACCGCGGTG 484
Qy 37 -----GlnPhePheAlaHisGlyAsnHisHisHisHisHisHisGlySerAlaAla 53.
Db 485 ACTCAGATGAGCTGGCGCGCGACGCTCACCAGCGACCATCACCACCATCACCACGATCA 544
Qy 54 AspTyrProValProProProProProProProProPheAspHisArgArgThrTrpThrArgPro 73
Db 545 -----CCGCGCGCG----- 553
Qy 74 PheHisGluThrAlaAlaGlyAsnSerArgLeuThrLeuGluValGlyAlaGly 93
Db 554 -----TCAGCGCTGCCAGTCCGCGCGACAGCTGCCACTAGTACCCGCGCGCG 604
Qy 94 GlyGlnHisMetAlaHisLeuValGlnProProAlaArgAlaHisIleValProPheTyr 113
Db 605 GGACCGCAC-----GGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 643
Qy 114 GlyGlyAlaPheThrAsnThrIleSerAsnGluAlaIleMetThrIleAspThrGluMet 133
Db 644 AACCGTAGTGTGGAGACCGCTTCTCTGACGACCGAGCTGGTGTCCATGTCCGTGCGTGAG 703
Qy 134 MetValGlyProAlaHisTyrProThrMetGlnGluArgAlaAlaLysValMetArgTyr 153
Db 704 CTGAACCGCCACCTCGCGGGCTTCCACGAGGAG-----GTGATCCCGCTG 751
Qy 154 ArgGluLysArg-----LysArgArgArgTyrAspLysGlnIleArgTyrGlu 169
Db 752 AAGCAGAAGCGCGCGACCCCTGAAGAACCGGGCTACGCCCATCGTCCGAGGTATATAA 808

RESULT 8
US-09-925-065A-586552/c
/ Sequence 586552, Application US/09925065A
/ Publication No. US20040181048A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single
/ Nucleotide Polymorphisms in the Human Genome
/ FILE REFERENCE: 108827.135
/ CURRENT APPLICATION NUMBER: US/09/925,065A
/ CURRENT FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: US 60/243,096
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 60/252,147
```

```
/ PRIOR FILING DATE: 2000-11-20
/ PRIOR APPLICATION NUMBER: US 60/250,092
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: US 60/261,766
/ PRIOR FILING DATE: 2001-01-16
/ PRIOR APPLICATION NUMBER: US 60/289,846
/ PRIOR FILING DATE: 2001-05-09
/ NUMBER OF SEQ ID NOS: 957086
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 586552
/ LENGTH: 507
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: misc feature
/ LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,
/ LOCATION: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31,
/ LOCATION: 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45,
/ LOCATION: 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59,
/ LOCATION: 60
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
/ LOCATION: 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89,
/ LOCATION: 90, 91, 92, 93, 94, 95, 96
/ OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-586552

Alignment Scores:
Pred. No.: 0.00779 Length: 507
Score: 125.00 Matches: 20
Percent Similarity: 62.5% Conservative: 5
Best Local Similarity: 50.0% Mismatches: 11
Query Match: 11.9% Indels: 5
DB: 6 Gaps: 1

US-10-723-947-77 (1-187) x US-09-925-065A-586552 (1-507)

Qy 22 HisHisHisHisHisHisHisGlnGluHisGlnLeuGlyGlnPhePheAlaHis 41
Db 222 CACCACCATCACCACCATCACCATAAACCAACCAACCAACCAACCACTACTACCAAC 163
Qy 42 GlyAsnHisHisHisHisHisHisGlySerAlaAlaAspTyrProValProProPro 61
Db 162 CACCACCATCACCACCATCACCACCA-----CTACCACCTACCACCAACCA 116

RESULT 9
US-10-995-561-13269
/ Sequence 13269, Application US/10995561
/ Publication No. US20050272054A1
/ GENERAL INFORMATION:
/ APPLICANT: Cargill, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
/ DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001559
/ CURRENT APPLICATION NUMBER: US/10/995,561
/ CURRENT FILING DATE: 2004-11-24
/ NUMBER OF SEQ ID NOS: 85702
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13269
/ LENGTH: 63693
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ NAME/KEY: misc feature
/ LOCATION: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17,
/ LOCATION: 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31,
/ LOCATION: 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45,
/ LOCATION: 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59,
/ LOCATION: 60
/ OTHER INFORMATION: n = A,T,C or G
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75,
/ LOCATION: 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89,
/ LOCATION: 90, 91, 92, 93, 94, 95, 96
/ OTHER INFORMATION: n = A,T,C or G
US-09-925-065A-586552

Alignment Scores:
Pred. No.: 1.38 Length: 63693
Score: 125.00 Matches: 32
Percent Similarity: 37.4% Conservative: 11
Best Local Similarity: 27.8% Mismatches: 40
Query Match: 11.9% Indels: 32
```


[illegible][illegible]

Search completed: February 23, 2006, 12:07:53
Job time : 1579 secs

```

RESULT 15
US-09-925-065A-48800/c
; Sequence 48800, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24

```

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☐ BLACK BORDERS

☒ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES

☐ FADED TEXT OR DRAWING

☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING

☐ SKEWED/SLANTED IMAGES

☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS

☐ GRAY SCALE DOCUMENTS

☐ LINES OR MARKS ON ORIGINAL DOCUMENT

☒ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.